

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 14:32:43 ; Search time 12601.5 Seconds
(without alignments)
17976.355 Million cell updates/sec

Title: US-09-497-957-1

Perfect score: 10825
Sequence: 1 TCTAGAGTTGAGATAAAATT.....TCCCCAAATTTTCATAAAC 10825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
- 1: gb.ba.*
 - 2: gb.htg.*
 - 3: gb.in.*
 - 4: gb.om.*
 - 5: gb.ov.*
 - 6: gb.pat.*
 - 7: gb.ph.*
 - 8: gb.pl.*
 - 9: gb.pr.*
 - 10: gb.ro.*
 - 11: gb.sts.*
 - 12: gb.sy.*
 - 13: gb.un.*
 - 14: gb.vi.*
 - 15: em.ba.*
 - 16: em.fun.*
 - 17: em.hum.*
 - 18: em.in.*
 - 19: em.mu.*
 - 20: em.om.*
 - 21: em.or.*
 - 22: em.ov.*
 - 23: em.pat.*
 - 24: em.ph.*
 - 25: em.pl.*
 - 26: em.to.*
 - 27: em.sts.*
 - 28: em.un.*
 - 29: em.vi.*
 - 30: em.htg_hum.*
 - 31: em.htg_inv.*
 - 32: em.htg_other.*
 - 33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description

1	10823	100.0	10825	6	AR117789
2	10823	100.0	10825	6	AR117790
3	10823	100.0	10825	6	AR117791
4	10823	100.0	10825	6	AR117792
5	10823	100.0	10825	6	AR149459
6	10823	100.0	10825	6	AR149460
7	10823	100.0	10825	6	AR149461
8	10823	100.0	10825	6	AR149462
9	10823	100.0	246240	6	AR036572
10	10823	100.0	246240	6	AR036573
11	10823	100.0	246240	6	AR036574
12	10759.8	99.4	12146	9	HSHE
13	10658.6	98.5	193752	2	AL359892
14	7542	69.7	246282	9	HSU01328
15	4251	39.3	101099	9	AL353759
16	2556.4	23.6	8622	6	AX347044
17	2248.8	20.8	8622	6	AX347045
18	1508.6	13.9	2115	9	HSA404378
19	1421	13.1	1479	9	HSHLAA6
20	1407	13.0	4349	4	AF301592
21	1051.6	9.7	2727	9	HSU60319
22	1030.2	9.5	1885	9	AF144242
23	831.2	7.7	874	9	HSHLAH2
24	769.4	7.1	772	9	AF184234
25	740.2	6.8	3334	4	AF301591
26	701	6.5	701	9	HSA298859
27	677.8	6.3	794	9	AF144238
28	657	6.1	761	9	HSHLAH1
29	638.4	5.9	653	9	HSHLAH4
30	560	5.2	560	9	HSA298840
31	547	5.1	547	9	AF147392
32	546.8	5.1	551	9	AF331065
33	516	4.8	517	6	AR117804
34	516	4.8	517	6	AR117805
35	516	4.8	517	6	AR149474
36	516	4.8	517	6	AR149475
37	516	4.8	517	6	182157
38	516	4.8	517	6	182158
39	516	4.8	517	6	182167
40	511.6	4.7	526	9	HSHLAH7
41	430.2	4.0	987	9	AF150664
42	398.2	3.7	128726	9	AL136458
43	398.2	3.7	130195	2	AC090170
44	393.8	3.6	103259	2	AC012430
45	389	3.6	190112	2	AP002354

ALIGNMENTS

RESULT	1				
AR117789	LOCUS	AR117789	10825 bp	DNA	linear
	DEFINITION	Sequence 1 from patent US 6140305.			PAT 16-MAY-2001
	ACCESSION	AR117789			
	VERSION	AR117789.1	GI:14098695		
	KEYWORDS	Unknown.			
	SOURCE	Unknown.			
	ORGANISM	Unclassified.			
	REFERENCE	1 (bases 1 to 10825)			
	AUTHORS	Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., Tsuchihashi, Z. and Wolff, R.K.			
	TITLE	Hereditary hemochromatosis gene products			
	JOURNAL	Patent: US 6140305-A 1 31-OCT-2000;			
	FEATURES	Location/Qualifiers			
	source	1. 10825			
	BASE COUNT	2998 a	2253 c	2648 g	2926 t
	ORIGIN				
	Query Match		Score 10823;	DB 6;	Length 10825;
			100.0%;		

Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTAAGGTGAGATAAAATTTTAAATGTATGATGAAATTTTGAAATCATATAATATTTA 60
Db 1 TCTAAGGTGAGATAAAATTTTAAATGTATGATGAAATTTTGAAATCATATAATATTTA 60
Qy 61 AATATCTAAAGTTCAGATCAGACATTCGCAAGCTACTTTCCCAATCAACAACCCCT 120
Db 61 AATATCTAAAGTTCAGATCAGACATTCGCAAGCTACTTTCCCAATCAACAACCCCT 120
Qy 121 TCAGGATTTAAAAACCAAGGGGACACTGGATCACCCTAGTGTGTTTCAACAAGCAGGTACCTT 180
Db 121 TCAGGATTTAAAAACCAAGGGGACACTGGATCACCCTAGTGTGTTTCAACAAGCAGGTACCTT 180
Qy 181 CTGCTGTAGGAGAGAGAACTAAAGTCTTGAAGACCTGTTTCCACAGGAAGTT 240
Db 181 CTGCTGTAGGAGAGAGAACTAAAGTCTTGAAGACCTGTTTCCACAGGAAGTT 240
Qy 241 TTTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTTGAGGCCATCCCCG 300
Db 241 TTTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTTGAGGCCATCCCCG 300
Qy 301 TTTCCCGCCGCCCAAGAGAGCGAGATTTAAGCGGGAGCTGGCGCCAGAGCTGGGGAA 360
Db 301 TTTCCCGCCGCCCAAGAGAGCGAGATTTAAGCGGGAGCTGGCGCCAGAGCTGGGGAA 360
Qy 361 ATGGGCGCGGAGCGAGCGCGGCGCTCTCTCTCTGATGTTTTCAGAGCGGGGCTCTG 420
Db 361 ATGGGCGCGGAGCGAGCGCGGCGCTCTCTCTCTGATGTTTTCAGAGCGGGGCTCTG 420
Qy 421 CAGGGCGGCTTGTCTGCTGAGTCCAGGGCTGCGGGGCACTAGGGCGGGGGGGTG 480
Db 421 CAGGGCGGCTTGTCTGCTGAGTCCAGGGCTGCGGGGCACTAGGGCGGGGGGGTG 480
Qy 481 GAAATCGAACTAGCTTTTCTTGGCTTGGAGTTTCTTAACCTTGGAGACCTGC 540
Db 481 GAAATCGAACTAGCTTTTCTTGGCTTGGAGTTTCTTAACCTTGGAGACCTGC 540
Qy 541 TCAACCCCTATCCGGAAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGAGGAGTGC 600
Db 541 TCAACCCCTATCCGGAAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGAGGAGTGC 600
Qy 601 CTACCACTGAAGTGCAGATAGGGTCCCTCGCCAGACCTGCCCCCTCCCGGGCTGT 660
Db 601 CTACCACTGAAGTGCAGATAGGGTCCCTCGCCAGACCTGCCCCCTCCCGGGCTGT 660
Qy 661 CCGGCTCTGCGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCCCACTAGAATGCTTT 720
Db 661 CCGGCTCTGCGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCCCACTAGAATGCTTT 720
Qy 721 TAAATAAATCTCGTAGTTCCTCAGTGTAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG 780
Db 721 TAAATAAATCTCGTAGTTCCTCAGTGTAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG 780
Qy 781 AACTCGGGTTTATTTCCAAATGTACGTGTGCAATTTTTCCTCCAGTCACTCCCAACAGG 840
Db 781 AACTCGGGTTTATTTCCAAATGTACGTGTGCAATTTTTCCTCCAGTCACTCCCAACAGG 840
Qy 841 AAGTTCCTCCCTGAGTGTGCTGCGGAGAGGCTGAGCAACCCACAGAGATCCGACGG 900
Db 841 AAGTTCCTCCCTGAGTGTGCTGCGGAGAGGCTGAGCAACCCACAGAGATCCGACGG 900
Qy 901 GGTTCACACTCAGAACGAATGGTGGCGGTGGGGCGGCAAGAGTGGGGTGGGGA 960
Db 901 GGTTCACACTCAGAACGAATGGTGGCGGTGGGGCGGCAAGAGAGTGGGGTGGGGA 960
Qy 961 TCTGAATTTCTACCAATTCACCCACTTTTGGTGTAGACCTGGGGTGGAGTCTAGGGT 1020
Db 961 TCTGAATTTCTACCAATTCACCCACTTTTGGTGTAGACCTGGGGTGGAGTCTAGGGT 1020
Qy 1021 GGGAGGCTCTGTAGAGAGGCTACTCTCGGGGCTTTCCCACTCTTGGCAATTTGTTCTTT 1080
Db 1021 GGGAGGCTCTGTAGAGAGGCTACTCTCGGGGCTTTCCCACTCTTGGCAATTTGTTCTTT 1080

Db 1021 GGGAGGCTCTGTAGAGAGGCTACTCTCGGGGCTTTCCCACTCTTGGCAATTTGTTCTTTT 1080
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Db 1081 GCCTGGAATAATTAAGTATATATGTAGTGTGAAAGCTTTGAACTGAACAATCTCTTTTCGG 1140
Qy 1141 CTAGGCTTTATTTGATTTGCAATGTGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200
Db 1141 CTAGGCTTTATTTGATTTGCAATGTGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200
Qy 1201 TAATGAACATGTAAAGCAATGCACTCACTTCTAAGTTACATTCATATCTGATCTTATTTGA 1260
Db 1201 TAATGAACATGTAAAGCAATGCACTCACTTCTAAGTTACATTCATATCTGATCTTATTTGA 1260
Qy 1261 TTTTCACTAGGCAATAGGAGGTAGGAGCTTAATAACGTTATTTTACTAGAAGTTAACT 1320
Db 1261 TTTTCACTAGGCAATAGGAGGTAGGAGCTTAATAACGTTATTTTACTAGAAGTTAACT 1320
Qy 1321 GGAATTCAGATTTATTAAGTCTTTTTCAGTTTACAAGAACATATAATCTGGTTCCTG 1380
Db 1321 GGAATTCAGATTTATTAAGTCTTTTTCAGTTTACAAGAACATATAATCTGGTTCCTG 1380
Qy 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTTAGTTGACAGTGAATTTGCCCTGTAG 1440
Db 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTTAGTTGACAGTGAATTTGCCCTGTAG 1440
Qy 1441 TGTAGCACAGTGTCTGTGGGTACACGCGGCTCAGCACAGACACTTTGAGTTTGGTA 1500
Db 1441 TGTAGCACAGTGTCTGTGGGTACACGCGGCTCAGCACAGACACTTTGAGTTTGGTA 1500
Qy 1501 CTACGTGTATCCACATTTTACACATGACAAAGATGAGGCAATGAGGCTGCTTCCCTGG 1560
Db 1501 CTACGTGTATCCACATTTTACACATGACAAAGATGAGGCAATGAGGCTGCTTCCCTGG 1560
Qy 1561 CAAATTTTCAATGTGTACACTGGGCTTTGGTGGCAGAGCTCATGCTCCACTTCAATAGC 1620
Db 1561 CAAATTTTCAATGTGTACACTGGGCTTTGGTGGCAGAGCTCATGCTCCACTTCAATAGC 1620
Qy 1621 TATGATTTTAAACATCAGACTGCAATAGAGGTTGAATATAAATTTTCATGTTGAGCAG 1680
Db 1621 TATGATTTTAAACATCAGACTGCAATAGAGGTTGAATATAAATTTTCATGTTGAGCAG 1680
Qy 1681 AAATATTCATTTGTTTACAAAGTGTAAATGATCCCAAGCAATGTGTCACACTGTTCAAGCC 1740
Db 1681 AAATATTCATTTGTTTACAAAGTGTAAATGATCCCAAGCAATGTGTCACACTGTTCAAGCC 1740
Qy 1741 CAAGGGAGAGCAGGAGAAACAGTCTTTACCCCTTTTATTTGATTTTTCATTTCTAGTGGGAGA 1800
Db 1741 CAAGGGAGAGCAGGAGAAACAGTCTTTACCCCTTTTATTTGATTTTTCATTTCTAGTGGGAGA 1800
Qy 1801 GATGACAATAAGCAAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 1860
Db 1801 GATGACAATAAGCAAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA 1860
Qy 1861 GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGCTGACACTTCAGCAGAGACATGAAGGA 1920
Db 1861 GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGCTGACACTTCAGCAGAGACATGAAGGA 1920
Qy 1921 AATAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGCGCAAG 1980
Db 1921 AATAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGCGCAAG 1980
Qy 1981 TTGGATTTAAAGCGGTTTTCAGCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
Db 1981 TTGGATTTAAAGCGGTTTTCAGCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
Qy 2041 CGGCGTGGGGTGGGAAGGGGACTACCATCTAGGATCTCTAGCAGTATCTCTGT 2100
Db 2041 CGGCGTGGGGTGGGAAGGGGACTACCATCTAGGATCTAGGATCTCTAGCAGTATCTCTGT 2100
Qy 2101 CCTCCCTACTCAGTGTGTGTAGGAGCAGTCCCCAGTCTTGACAAACCAAAATGTCTCT 2160
Db 2101 CCTCCCTACTCAGTGTGTGTAGGAGCAGTCCCCAGTCTTGACAAACCAAAATGTCTCT 2160

QY 2161 AAACCTTTGCCACATGTCACCTAGTAGACAAACCTCTCGTTAAGAAGCTCGGGTTGAAAA 2220
DB 2161 AAACCTTTGCCACATGTCACCTAGTAGACAAACCTCTCGTTAAGAAGCTCGGGTTGAAAA 2220
QY 2221 AATAAACAAGTACTGCTGGGAGTAGAGCCAAAGAAGTAGTAAATGGGCTCACAAGAGA 2280
DB 2221 AATAAACAAGTACTGCTGGGAGTAGAGCCAAAGAAGTAGTAAATGGGCTCACAAGAGA 2280
QY 2281 GCCAACAAGGTTGTGCAGCGGCTGTAGGCTGTGGTGAATTCAGCCAAGAGTA 2340
DB 2281 GCCAACAAGGTTGTGCAGCGGCTGTAGGCTGTGGTGAATTCAGCCAAGAGTA 2340
QY 2341 ACAGTGATCTGTACACAGGCTTTTAAAGATTGCTCTGCCTGCTATGTGGAACAGAAATG 2400
DB 2341 ACAGTGATCTGTACACAGGCTTTTAAAGATTGCTCTGCCTGCTATGTGGAACAGAAATG 2400
QY 2401 AAGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAGAGCTGTACACAGTCCAGGCAAG 2460
DB 2401 AAGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAGAGCTGTACACAGTCCAGGCAAG 2460
QY 2461 AGGTAGTGGAGTGGGCTGGGACAGAAAGGGAGTGACAAACCATTTGCTCTCTGAA 2520
DB 2461 AGGTAGTGGAGTGGGCTGGGACAGAAAGGGAGTGACAAACCATTTGCTCTCTGAA 2520
QY 2521 TATATCTGAAGAAAGTCTCTGAAGATTCTATGTGTGAGAGAAAGAGAAATGG 2580
DB 2521 TATATCTGAAGAAAGTCTCTGAAGATTCTATGTGTGAGAGAAAGAGAAATGG 2580
QY 2581 CTGGGTGTAGTACTCATGCCAAGAGAGAGGCCAAGAGAGCAGATTCTGAGCTCAGGA 2640
DB 2581 CTGGGTGTAGTACTCATGCCAAGAGAGAGGCCAAGAGAGCAGATTCTGAGCTCAGGA 2640
QY 2641 GTTCAAGACAGCCTGGGCAACACAGCAAAACCCCTCTCTACAAAAATACAAAAATTA 2700
DB 2641 GTTCAAGACAGCCTGGGCAACACAGCAAAACCCCTCTCTACAAAAATACAAAAATTA 2700
QY 2701 GCTGGGTGTGGCATGCACCTGTATCTAGCTAGCTACCTCGGAGGCTGAGGTGAGGGTA 2760
DB 2701 GCTGGGTGTGGCATGCACCTGTATCTAGCTAGCTACCTCGGAGGCTGAGGTGAGGGTA 2760
QY 2761 TTGCTTGAGCCCAAGAGTTGAGGCTGCAGTGCATGAGCTGTGCACGTGACTGTACTCAGC 2820
DB 2761 TTGCTTGAGCCCAAGAGTTGAGGCTGCAGTGCATGAGCTGTGCACGTGACTGTACTCAGC 2820
QY 2821 CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAGAGAGAGCTTAAAGT 2880
DB 2821 CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAGAGAGAGCTTAAAGT 2880
QY 2881 TGACTTTGTCTTTATTTTAAATTTATTTGGCTGAGCAGTGGGGTAAATGGCAATGCCAT 2940
DB 2881 TGACTTTGTCTTTATTTTAAATTTATTTGGCTGAGCAGTGGGGTAAATGGCAATGCCAT 2940
QY 2941 TTCTGAGATGGTGAAGGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGAGATCTGCAATTTG 3000
DB 2941 TTCTGAGATGGTGAAGGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGAGATCTGCAATTTG 3000
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DB 3001 GGACATGTTAAGTTTGAGATTCCAGTCAAGGCTTCCAGTGTGAGGCCACATAGGCAGTT 3060
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DB 3061 CAGTGTGAAGAAATTCAGGACCAAGGCTGGGACGGTGGCTGCTCTGCTAATCCAGCACT 3120
QY 3121 TTGCTGCTGAGGCAGGTAGATCAATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCCAACA 3180
DB 3121 TTGCTGCTGAGGCAGGTAGATCAATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCCAACA 3180
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DB 3181 TGGTGAACCCCATGCTACTAAAAATACAAAAATACAAAAATACAAAAATACAAAAATAC 3240

QY 3241 ATAGTCCCAGGTTTTACGAGGCTTAGGTAGGAAATCCCTTGAACCCAGGAGGTGCAGG 3300
DB 3241 ATAGTCCCAGGTTTTACGAGGCTTAGGTAGGAAATCCCTTGAACCCAGGAGGTGCAGG 3300
QY 3301 TTGCACTGAGCTGAGATTGTCCCACTGCACCTCCAGGCTGGGTGATAGAGTGAGACTCTGT 3360
DB 3301 TTGCACTGAGCTGAGATTGTCCCACTGCACCTCCAGGCTGGGTGATAGAGTGAGACTCTGT 3360
QY 3361 CTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3420
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QY 3421 TCTTAATTTGCCCTGAGCACCACCTCTGAGTTCAACTACCATGGCTAGACACACCTTAAC 3480
DB 3421 TCTTAATTTGCCCTGAGCACCACCTCTGAGTTCAACTACCATGGCTAGACACACCTTAAC 3480
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DB 3541 CTGGGGCAGTGAAGGGGTGGCAGCCACGTGTGGCAGAGAAAGCACACAGAAAGAGC 3600
QY 3601 ACCCAGGACTGTATATGGAAGAAAGACAGACTGCAACTCAACCTTCAAAAAATGAGGA 3660
DB 3601 ACCCAGGACTGTATATGGAAGAAAGACAGACTGCAACTCAACCTTCAAAAAATGAGGA 3660
QY 3661 CCAGACACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
DB 3661 CCAGACACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
QY 3721 CTCTACTACACATGTTAAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 3780
DB 3721 CTCTACTACACATGTTAAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 3780
QY 3781 CTCTCTAGTGGTGCCTCAGACAGGACCTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3840
DB 3781 CTCTCTAGTGGTGCCTCAGACAGGACCTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3840
QY 3841 CGTGGATGACACAGCTGTTGTTCTATGATNATGAGATGCGCGGTGGAGCCCGCAAC 3900
DB 3841 CGTGGATGACACAGCTGTTGTTCTATGATCATGAGATGCGCGGTGGAGCCCGCAAC 3900
QY 3901 TCCATGGGTTTTCCAGTAGAATTTCAAGCCAGATGTGCTGCAGTGCAGTGCAGTGCAGT 3960
DB 3901 TCCATGGGTTTTCCAGTAGAATTTCAAGCCAGATGTGCTGCAGTGCAGTGCAGTGCAGT 3960
QY 3961 AGGTTGGGATCACATGTTCACTGTTGACTTCTGGACTATATGGAATAATCACACACAG 4020
DB 3961 AGGTTGGGATCACATGTTCACTGTTGACTTCTGGACTATATGGAATAATCACACACAG 4020
QY 4021 CAAGGATGTGGAGAGGGGCTCACCTTCTCAGGTTGTGAGAGCTTTTTCATCTTTTC 4080
DB 4021 CAAGGATGTGGAGAGGGGCTCACCTTCTCAGGTTGTGAGAGCTTTTTCATCTTTTC 4080
QY 4081 ATGCACTTTGAAGAAACAGCTGCAAGTCTGAGTCTTGTGGAGCAGGAGAGAGAG 4140
DB 4081 ATGCACTTTGAAGAAACAGCTGCAAGTCTGAGTCTTGTGGAGCAGGAGAGAGAGAG 4140
QY 4141 GAATTTGCTTCTGAGATCATTTTGGTGGGATGGTGGAAATAGGAGCCTATTCCTT 4200
DB 4141 GAATTTGCTTCTGAGATCATTTTGGTGGGATGGTGGAAATAGGAGCCTATTCCTT 4200
QY 4201 TGGTTCAGTTAAACAGGCTGGGATTTTCCAGAGTCCACACCTGCGAGTCACTCTG 4260
DB 4201 TGGTTCAGTTAAACAGGCTGGGATTTTCCAGAGTCCACACCTGCGAGTCACTCTG 4260
QY 4261 GCGTGTGAATCCAGAGAGACACAGTACCGAGGCTTACTGGAAGTACGGGTATGATGGG 4320
DB 4261 GCGTGTGAATCCAGAGAGACACAGTACCGAGGCTTACTGGAAGTACGGGTATGATGGG 4320
QY 4321 CAGGACCACTTGAATTTCTGCCCTGACACACTGGAATGGAGAGCAGACAGACCCAGGCC 4380

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Db 4321 CAGGACCCTGATCTGCTCCCTGACACACTGGATTGGAGGACGACAGACCCAGGGCC 4380
QY 4381 TGGCCCAACAAGCTGGAGTGGGAAGGCAACAAGATTGGGGCCAGGCAAGAGGCCCTAC 4440
Db 4381 TGGCCCAACAAGCTGGAGTGGGAAGGCAACAAGATTGGGGCCAGGCAAGAGGCCCTAC 4440
QY 4441 CTGGAGAGGAGTGGCCCTGACAGCTGCAGCAGTTCCTGGAGTGGGGAGAGGCTTTTG 4500
Db 4441 CTGGAGAGGAGTGGCCCTGACAGCTGCAGCAGTTCCTGGAGTGGGGAGAGGCTTTTG 4500
QY 4501 GACCAACAAGGTATGGTGGAAACACACTTCCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560
Db 4501 GACCAACAAGGTATGGTGGAAACACACTTCCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560
QY 4561 AGGTTGCAAGGACAGGATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 4620
Db 4561 AGGTTGCAAGGACAGGATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 4620
QY 4621 TCCAAATTCGGGAGGAGCTTCTCAATCCTAGAGTCTACCTTATATAGATGTA 4680
Db 4621 TCCAAATTCGGGAGGAGCTTCTCAATCCTAGAGTCTACCTTATATAGATGTA 4680
QY 4681 TGAGACGCCACAAGTCATGGGTTTAATTTCTTTCTCCATGCATATGGCTCAAAAGGAA 4740
Db 4681 TGAGACGCCACAAGTCATGGGTTTAATTTCTTTCTCCATGCATATGGCTCAAAAGGAA 4740
QY 4741 GTGTCTATGGCCCTGTCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA 4800
Db 4741 GTGTCTATGGCCCTGTCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA 4800
QY 4801 AAATTCAGAAATGCAAGCGGGGACGGTGGCTACCCCTGTATTCGACGACCTTTGGG 4860
Db 4801 AAATTCAGAAATGCAAGCGGGGACGGTGGCTACCCCTGTATTCGACGACCTTTGGG 4860
QY 4861 AGGCGGAGCGGGTGGTCACAAGGTGAGGAGTTTGAGACGACGCTGACCAACATGGTAA 4920
Db 4861 AGGCGGAGCGGGTGGTCACAAGGTGAGGAGTTTGAGACGACGCTGACCAACATGGTAA 4920
QY 4921 ACCCGTCTTAATAAATAACAAAATTTAGCTGGTCACAGTCATCGCCACCTGTAGTCCCA 4980
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QY 4981 GCTAATTTGGAAGGCTGAGGCAAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACATGA 5040
Db 4981 GCTAATTTGGAAGGCTGAGGCAAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACATGA 5040
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Db 5041 GCCAAGATCGGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAAA 5100
QY 5101 AAAAAAATAAAGAGAGAAATTCAGAGATCTCAGCTATCATATGAATPACGAGACAAA 5160
Db 5101 AAAAAAATAAAGAGAGAAATTCAGAGATCTCAGCTATCATATGAATPACGAGACAAA 5160
QY 5161 ATATCAAGTGAGGCGACCTATCAGATAGAAAGTCCCTTTAGTTTAAAGTTTCTTTTCAT 5220
Db 5161 ATATCAAGTGAGGCGACCTATCAGATAGAAAGTCCCTTTAGTTTAAAGTTTCTTTTCAT 5220
QY 5221 AGAATATAGCAATATCTAGAGCTACCTATCTTACAAGTCGGCTTCTTATACAATGC 5280
Db 5221 AGAATATAGCAATATCTAGAGCTACCTATCTTACAAGTCGGCTTCTTATACAATGC 5280
QY 5281 CTCCTAGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGCACATAA 5340
Db 5281 CTCCTAGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGCACATAA 5340
QY 5341 AGGGCAATTTTATCTATCAGAACAAAGACATGGGTAAACAGATATGTATATTACATGTG 5400
Db 5341 AGGGCAATTTTATCTATCAGAACAAAGACATGGGTAAACAGATATGTATATTACATGTG 5400
QY 5401 AGGAGAACAGCTGATCTGCTCTCCCAAGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460
|||||

Db 5401 AGGAGAACAGCTGATCTGACTGCTCCAGGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460
QY 5461 ACACAAAATGGTGTCTCTCTCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTCTCTCTCC 5520
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ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas W.J., Drayna D.T., Feder J.N., Gnirke A., Ruddy D.,
Tsuchihashi Z., and Wolffe R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 3 31-Oct-2000;
FEATURES Location/Qualifiers
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BASE COUNT 2999 a 2253 c 2647 g 2926 t
ORIGIN

Query Match 100.0%; Score 10823; DB 6; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS AR117792
DEFINITION Sequence 7 from patent US 6140305.
ACCESSION AR117792
VERSION AR117792.1 GI:14098698
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Dryana,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 7 31-OCT-2000;
FEATURES
source 1. 10825
/organism="unknown"
BASE COUNT 2999 a 2252 c 2648 g 2926 t
ORIGIN

Query Match 100.0%; Score 10823; DB 6; Length 10825;
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RESULT 5
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LOCUS AR149459
DEFINITION Sequence 1 from patent US 6228594.
ACCESSION AR149459
VERSION AR149459.1 GI:15114050
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,

Tsuchihashi,2. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 1 08-MAY-2001;
JOURNAL Location/Qualifiers
FEATURES
source 1..10825
BASE COUNT 2998 a 2253 c 2648 g 2926 t
ORIGIN
Query Match 100.0%; Score 10823; DB 6; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TCTAAGGTGAGATAAAATTTTAAATGTATGATGAATTTTGAATAATCATAAATATTTA 60
Db 1 TCTAAGGTGAGATAAAATTTTAAATGTATGATGAATTTTGAATAATCATAAATATTTA 60
Qy 61 AATATCTAAAGTTTCAGATCAGAACATTTGCGRAGTACTTTCCCAATCAACAACCCCT 120
Db 61 AATATCTAAAGTTTCAGATCAGAACATTTGCGRAGTACTTTCCCAATCAACAACCCCT 120
Qy 121 TCAGGATTTAAACCAAGGGGACACTGGATCACTAGTGTTCACAGCAGGTACCTT 180
Db 121 TCAGGATTTAAACCAAGGGGACACTGGATCACTAGTGTTCACAGCAGGTACCTT 180
Qy 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTCTTTTACCAGGAAGTT 240
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Qy 241 TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGGAGCATCCCG 300
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Qy 361 ATGGGCGCGGAGCCAGCGCGCTTCCTCCTGATGCTTTTTCAGACCGCGTCTG 420
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Qy 421 CAGGGCGCTTGTGCTGAGTCCGAGGCTCGGGCGCAACTAGGGGCGCGGGGGTG 480
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Qy 481 GAAAAATCGAACTAGCTTTTCTTGGCCTTGGGAGTTTGCTAACTTTGGAGACCTGC 540
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Qy 841 AAGTCTTCTCCCTGAGTGTGCGGAGAAAGCTGAGCAAAACCCACAGCAGATCCGACAGG 900
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Qy	3061	CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCACGGTGGCTCACCTTCGTGTAATCCAGCACT	3120
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Qy	3121	TTGGTGGCTTGAGCGCAGGTAGATCATTTTCAGGTGCAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
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Qy	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGGTGGCGCAGCGCT	3240
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Qy	3241	ATAGTCCCGAGTTTTCAGGAGGCTTAGTAGAGAAATCCCTTGAACCCAGGAGTGCAGG	3300
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Qy	3481	ATTTTCTAGAAATCCACACGCTTTAGTGGAGTCTGTCTTAATCATGAGTATTTGGAATAGGAT	3540
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Qy	3541	CTGGGGCAGCTGAGGGGTGGCAGGCACAGCTGTGGCAGAGAAAACACACAAGAAAAGAGC	3600
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Qy	3661	CCAGCACAGCTGATGGTATGAGTTGATGACGGTGTGTGGAGCGCTCAACAATCCTGCTCCC	3720
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Qy	3721	CTCTACTACACATGGTTAAGCGCTGTGCTCTGCTCCAGGTTTCACACTCTCTGCACTA	3780
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Qy	3721	CTCTACTACACATGGTTAAGCGCTGTGCTCTGCTCCAGGTTTCACACTCTCTGCACTA	3780
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Qy	3781	CCTCTTCATGGTGCCTCAGACAGAGACCTTGCTCTTCCCTTTGTAAGCTTTGGGCTA	3840
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Qy	3781	CCTCTTCATGGTGCCTCAGACAGAGACCTTGCTCTTCCCTTTGTAAGCTTTGGGCTA	3840
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Qy	3841	CGTGGATGACCAGCTGTTCTGTTCTATGATNATGAGAGTGCCTGTGGAGCCCCGAAAC	3900
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Qy	3841	CGTGGATGACCAGCTGTTCTGTTCTATGATNATGAGAGTGCCTGTGGAGCCCCGAAAC	3900
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Qy	3901	TCCATGGGTTTCCAGTAGAATTTCAACGCAGATGTGGCTGCAGCTGAGTCAAGTCTGAA	3960
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Qy	3901	TCCATGGGTTTCCAGTAGAATTTCAACGCAGATGTGGCTGCAGCTGAGTCAAGTCTGAA	3960
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Qy	3961	AGGTTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAATAATCAACAACACAG	4020
Db			
Qy	3961	AGGTTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAATAATCAACAACACAG	4020
Db			
Qy	4021	CAAGGGTATGTGGAGAGGGGGCCTCACCTTCCTGAGGTGTGCAGAGCTTTTCATCTTTTC	4080
Db			
Qy	4021	CAAGGGTATGTGGAGAGGGGGCCTCACCTTCCTGAGGTGTGCAGAGCTTTTCATCTTTTC	4080
Db			
Qy	4081	ATGCATCTTGAAGAAACACCTGAGTCTGTGAGTCTTGTGGGACACGGAGAGGGAAG	4140
Db			
Qy	4081	ATGCATCTTGAAGAAACACCTGAGTCTGTGAGTCTTGTGGGACACGGAGAGGGAAG	4140
Db			
Qy	4141	GAATTTTGCTCCTCAGATCATTTTGGTCCCTTGGGGATGTGGAAATAGGGAATATTCCTT	4200

Db	4141	GAATTTGCTCTCTTGAGATCATTTTGGTCCCTTGGGATGCTGGAATAGGGACCTATTCCCTT	4200
Qy	4201	TGGTTGCAGTTAAACAAGCTGGGGATTTTCCAGAGTCCCAACACCCCTGCAGGTCACTCCTG	4260
Db	4201	TGGTTGCAGTTAAACAAGCTGGGGATTTTCCAGAGTCCCAACACCCCTGCAGGTCACTCCTG	4260
Qy	4261	GGCTGTGAATGCAAGAACACACAGTACCGGAGGCTACTGGAAGTACGGGTATGATGGG	4320
Db	4261	GGCTGTGAATGCAAGAACACACAGTACCGGAGGCTACTGGAAGTACGGGTATGATGGG	4320
Qy	4321	CAGGACCACTTCAA'TCTGCCTGCACACTTGGATTGGAGAGCAGACAGAACCCAGGGCC	4380
Db	4321	CAGGACCACTTGAATCTGCCTGCACACTTGGATTGAGAGCAGACAGAACCCAGGGCC	4380
Qy	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCACAAGATTCCGGGCCAGCAGAACAGGGCCTAC	4440
Db	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCACAAGATTCCGGGCCAGCAGAACAGGGCCTAC	4440
Qy	4441	CTGGAGAGGACTGCCCTGCACAGCTGCACAGTTCCTGGAGCTGGGAGAGAGTGTTTTG	4500
Db	4441	CTGGAGAGGACTGCCCTGCACAGCTGCACAGTTCCTGGAGCTGGGAGAGAGTGTTTTG	4500
Qy	4501	GACCAACAAGTATGTTGGGAACACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560
Db	4501	GACCAACAAGTATGTTGGGAACACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560
Qy	4561	AGTTTCAGGGCACCGAATCCCTGGTTGCAGTTCAGAGTGGCTGAGGCTGTCTGCCTC	4620
Db	4561	AGTTTCAGGGCACCGAATCCCTGGTTGCAGTTCAGAGTGGCTGAGGCTGTCTGCCTC	4620
Qy	4621	TCCAAATCTGGGAAGGACTTTCTCAATCTCTAGAGTCTTACCTTATAATTTGAGATGTA	4680
Db	4621	TCCAAATCTGGGAAGGACTTTCTCAATCTCTAGAGTCTTACCTTATAATTTGAGATGTA	4680
Qy	4681	TGAGACAGCCACAAGTCATGGGTTTAA'TTCTTTTCTCCATGCATATGGCTCAAGGGAA	4740
Db	4681	TGAGACAGCCACAAGTCATGGGTTTAA'TTCTTTTCTCCATGCATATGGCTCAAGGGAA	4740
Qy	4741	GTGTCTATGGCCCTTGCTTTTTATTAAACAATAATCTTTTGTATATTATACCTGTAA	4800
Db	4741	GTGTCTATGGCCCTTGCTTTTTATTAAACAATAATCTTTTGTATATTATACCTGTAA	4800
Qy	4801	AAATTCAGAAATGTCAGGCGGGCAGGTGGCTCACCCCTGTATCCACGACTTTGGG	4860
Db	4801	AAATTCAGAAATGTCAGGCGGGCAGGTGGCTCACCCCTGTATCCACGACTTTGGG	4860
Qy	4861	AGGCGGAGGGGTGGTCACAAGCTCAGGAGTTTGAGACACCCCTGACCAACATGGTGAA	4920
Db	4861	AGGCGGAGGGGTGGTCACAAGCTCAGGAGTTTGAGACACCCCTGACCAACATGGTGAA	4920
Qy	4921	ACCCGCTCTTAAAAAATACAAAAATTTAGCTGGTACAGTCATGCGCAGCTGTAGTCCCA	4980
Db	4921	ACCCGCTCTTAAAAAATACAAAAATTTAGCTGGTACAGTCATGCGCAGCTGTAGTCCCA	4980
Qy	4981	GCTAATTCGAAGGCTGAGGAGGAGCATCCCTTGAACCTTGGGAAGGGAAGTTGACCTGA	5040
Db	4981	GCTAATTCGAAGGCTGAGGAGGAGCATCCGTTTGAACCTTGGGAAGGGAAGTTGACCTGA	5040
Qy	5041	GCCAAGATCGGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAA	5100
Db	5041	GCCAAGATCGGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAA	5100
Qy	5101	AAAAAATAAGGAGAAATTCAGAGATCTCAGCTATCATATGATACACAGACAAA	5160
Db	5101	AAAAAATAAGGAGAAATTCAGAGATCTCAGCTATCATATGATACACAGACAAA	5160
Qy	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCTTTAGTTAAAAAGTTCTTTTCAT	5220
Db	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCTTTAGTTAAAAAGTTCTTTTCAT	5220
Qy	5221	AGAACATAGCAATATACCTGAAGCTACCTATCTTACAAGTCGGTCTTATTAACATGTC	5280

DB	5221	AGACATAGCAATAACTACCTGAAGCTACCTATCTCTTACAAAGTCCCGCTCTCTTATAACAATGC	5281
QY	5281	CTCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCAITTTCAATGACACATAA	5340
DB	5281	CTCCTAGGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGACACATAA	5340
QY	5341	AGGCAATTTTATCTATCAGACAAGAACAATGCGGTACAGATATGTATAITTTACATGTG	5400
DB	5341	AGGCAATTTTATCTATCAGACAAGAACAATGCGGTACAGATATGTATAITTTACATGTG	5400
QY	5401	AGGAGAACAGCTGANTCTGACTCTCTCCAAAGTGACACTGTGTAGAGTCCAATCTTAGG	5460
DB	5401	AGGAGAACAGCTGANTCTGACTCTCTCCAAAGTGACACTGTGTAGAGTCCAATCTTAGG	5460
QY	5461	ACAAAAATGGTGCTCTCTCTGTAGCTTTCTTTTCTGAAAAGGGTATTTCCCTTCTCTCC	5520
DB	5461	ACAAAAATGGTGCTCTCTCTGTAGCTTTCTTTTCTGAAAAGGGTATTTCTTCTTCTCTCC	5520
QY	5521	AACCTATAGAAGAAAGTGAAGTTCCAGTCTTTCTTGGCAAGGGTAAACAGATCCCTCTC	5580
DB	5521	AACCTATAGAAGAAAGTGAAGTTCCAGTCTTTCTTGGCAAGGGTAAACAGATCCCTCTC	5580
QY	5581	CTCATCTCTCTCTTTCTTCTCAAGTGCCCTCTTTGGTGAAGGTGACACATCATGTGACC	5640
DB	5581	CTCATCTCTCTCTTTCTTCTCAAGTGCCCTCTTTGGTGAAGGTGACACATCATGTGACC	5640
QY	5641	TCCTCAGTGACCACTCTACGGTGTGGGGCTTTGAACCTACTACCCCAAGAACATCACCATTG	5700
DB	5641	TCCTCAGTGACCACTCTACGGTGTGGGGCTTTGAACCTACTACCCCAAGAACATCACCATTG	5700
QY	5701	AAGTGGCTGAAGGATGAAGCAGCAATGGATGCCAAGAGTTTCSAACCTTAAGACGTATTG	5760
DB	5701	AAGTGGCTGAAGGATGAAGCAGCAATGGATGCCAAGAGTTTCSAACCTTAAGACGTATTG	5760
QY	5761	CCCAATGGGATGGGACCTTACCAGGCTGGATTAACCTTTGGCTGTACCCCTGGGGAAGAG	5820
DB	5761	CCCAATGGGATGGGACCTTACCAGGCTGGATTAACCTTTGGCTGTACCCCTGGGGAAGAG	5820
QY	5821	CAGAGATATACGTTCCAGGTGGAGCACCCAGGCCCTGGATCAGCCCTCATTTGTGATCTGG	5880
DB	5821	CAGAGATATACGTTCCAGGTGGAGCACCCAGGCCCTGGATCAGCCCTCATTTGTGATCTGG	5880
QY	5881	GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTGAGAGGAGTGCC	5940
DB	5881	GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTGAGAGGAGTGCC	5940
QY	5941	TGAGGAGGTAATTTATGGCAGTGAGATGAGGATCTCTCTTTTGTAGGGGGTGGCTGAGG	6000
DB	5941	TGAGGAGGTAATTTATGGCAGTGAGATGAGGATCTCTCTTTTGTAGGGGGTGGCTGAGG	6000
QY	6001	GTGGCAATCAAAGGCTTTAACTTGCTTTTCTCTGTTTGAAGCCCTCACCCTCTGGCACCC	6060
DB	6001	GTGGCAATCAAAGGCTTTAACTTGCTTTTCTCTGTTTGAAGCCCTCACCCTCTGGCACCC	6060
QY	6061	TAGTCATTTGGAGTCATCAGTGGAAATGCTGTTTTTGTGCTCATCTTGTTCATTGGAAATTT	6120
DB	6061	TAGTCATTTGGAGTCATCAGTGGAAATGCTGTTTTTGTGCTCATCTTGTTCATTGGAAATTT	6120
QY	6121	TGTTTCAATAATTTAAGAAAGAGCGAGGTTCAAGTGAGTAGGAACAAGGGGGAGTCTCT	6180
DB	6121	TGTTTCAATAATTTAAGAAAGAGCGAGGTTCAAGTGAGTAGGAACAAGGGGGAGTCTCT	6180
QY	6181	TAGTACTCTTGCCCAAGGACAGGTGGAAGAGGGGACAGGGGATCTGGCATCCATGGG	6240
DB	6181	TAGTACTCTTGCCCAAGGACAGGTGGAAGAGGGGACAGGGGATCTGGCATCCATGGG	6240
QY	6241	AAGCATTTTCTCATTTATATTTCTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAAT	6300
DB	6241	AAGCATTTTCTCATTTATATTTCTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAAT	6300
QY	6301	AATGGTTCTCCCAAGAAAGTCTCTAATTCAAACAACATCTTCAGACACCTACTAT	6360
DB	6301	AATGGTTCTCCCAAGAAAGTCTCTAATTCAAACAACATCTTCAGACACCTACTAT	6360

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Db	6361	TTTCAAGAGCTGTTTAAGGTAGTACAGGGGCTTTTGAGTTGAGAAGTCACTGTGGCTAT	6420
Qy	6421	TCTCAGACCCAAATCTGTTAGGAATGAAATTCATACCAAGTAAATGTAGTTAAAGAG	6480
Db	6421	TCTCAGACCCAAATCTGTTAGGAATGAAATTCATACCAAGTAAATGTAGTTAAAGAG	6480
Qy	6481	ACCCCATGAGTCTTAAGCAGGACGAAAGCAAAATGCTTAGGGTCTCAAGGAAAGAAATG	6540
Db	6481	ACCCCATGAGTCTTAAGCAGGACGAAAGCAAAATGCTTAGGGTCTCAAGGAAAGAAATG	6540
Qy	6541	ATCACATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAGCTGGATTCCA	6600
Db	6541	ATCACATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAGCTGGATTCCA	6600
Qy	6601	TTAGGTGAGGTTGAAGATGATGGAGTCTACACAGACGAGCAACATGCCAAGTAGGA	6660
Db	6601	TTAGGTGAGGTTGAAGATGATGGAGTCTACACAGACGAGCAACATGCCAAGTAGGA	6660
Qy	6661	GAGTATAAGGCATCTACTGGGAGATTAGAAATAATTACTGTACCTTAACCCCTGAGTTTCGGT	6720
Db	6661	GAGTATAAGGCATCTACTGGGAGATTAGAAATAATTACTGTACCTTAACCCCTGAGTTTCGGT	6720
Qy	6721	AGCTATCACTCACCAATTATGCATTTCTACCCCTCGAACATCTGTGGTGTAGGGAAGA	6780
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Qy	6781	GAATCAGAAAGACCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA	6840
Db	6781	GAATCAGAAAGACCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA	6840
Qy	6841	TCACCTGGGTGTCATTGAGGATTCCTAAGAAAGGAGGACCAGATCTCCCTTATATGGTG	6900
Db	6841	TCACCTGGGTGTCATTGAGGATTCCTAAGAAAGGAGGACCAGATCTCCCTTATATGGTG	6900
Qy	6901	AATGTGTTGTTAAAGAGTTAGATGAGAGTGAGGAGACCAGTTAGAAAGCCCAATAAGCAT	6960
Db	6901	AATGTGTTGTTAAAGAGTTAGATGAGAGTGAGGAGACCAGTTAGAAAGCCCAATAAGCAT	6960
Qy	6961	TTCCAGATGAGAGTAAATGGTCTTGAAATCCAATAGTATGCCAGGTCTAAATTCAGATGG	7020
Db	6961	TTCCAGATGAGAGTAAATGGTCTTGAAATCCAATAGTATGCCAGGTCTAAATTCAGATGG	7020
Qy	7021	GTGAATGAGGAAATAAGGAAGAGAGCAAGATGGTGCCTTAGGTGTTGTGATGCCT	7080
Db	7021	GTGAATGAGGAAATAAGGAAGAGAGCAAGATGGTGCCTTAGGTGTTGTGATGCCT	7080
Qy	7081	CTTTCTCTGGTCTCTTGTTCCACAGGAGGAGCCATGGGGCACTACGCTTTAGCTGTAACG	7140
Db	7081	CTTTCTCTGGTCTCTTGTTCCACAGGAGGAGCCATGGGGCACTACGCTTTAGCTGTAACG	7140
Qy	7141	TGAGTGACGCGACCTGCAGACTACTGTGGGAAGGAGACAAACTAGAGACTCAAGA	7200
Db	7141	TGAGTGACGCGACCTGCAGACTACTGTGGGAAGGAGACAAACTAGAGACTCAAGA	7200
Qy	7201	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACTTAAACATAGAAATT	7260
Db	7201	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACTTAAACATAGAAATT	7260
Qy	7261	GCCTGAGCAACTCTTGATTTTAGCCTCTCTGTTCATTTCCCTCAAAAGAGATTTCCCAT	7320
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Db 8521 TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATAGAGAA 8580
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Db 8581 GGAAGGAGATGGCTTCTCTCTGTCTCATTTGTGTTTCTCTCTGAGTGAGCTTGAATCAAT 8640
QY 8641 GAAGGGAAACAGCAGAAAACCAACTGATCCTCAGCTGATGTTTCCCTTTAAAAATC 8700
Db 8641 GAAGGGAAACAGCAGAAAACCAACTGATCCTCAGCTGATGTTTCCCTTTAAAAATC 8700
QY 8701 CCTGAAGAAAGTCTGGAATGTGACTCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8760
Db 8701 CCTGAAGAAAGTCTGGAATGTGACTCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8760
QY 8761 TTTCTTTTGGACCCCTACGCAAGGACTGTAATTTGGTGGGACAGCTAGTGGCCCTCTGGC 8820
Db 8761 TTTCTTTTGGACCCCTACGCAAGGACTGTAATTTGGTGGGACAGCTAGTGGCCCTCTGGC 8820
QY 8821 TTCACACAGGTGTCTCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTCGTGGTATTT 8880
Db 8821 TTCACACAGGTGTCTCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTCGTGGTATTT 8880
QY 8881 CCTCAATGAAGTGGAGTAAGCTCTCATTTTGGATGGTATTAATGAAGCCACCAAGTG 8940
Db 8881 CCTCAATGAAGTGGAGTAAGCTCTCATTTTGGATGGTATTAATGAAGCCACCAAGTG 8940
QY 8941 GCTTAGAGGATGCCAGGTCTCTCCCTAGGCCACTCGGGTTCGGTGCGCATTTAAAAA 9000
Db 8941 GCTTAGAGGATGCCAGGTCTCTCCCTAGGCCACTCGGGTTCGGTGCGCATTTAAAAA 9000
QY 9001 AAAATCTAACAGGACATTCAGGAATTTGCTAGATTTCTGGAAATCAGTTTCACTATTT 9060
Db 9001 AAAATCTAACAGGACATTCAGGAATTTGCTAGATTTCTGGAAATCAGTTTCACTATTT 9060
QY 9061 AAAGAGTCTTTTTTTTTTTTTTTTGTGAGACTCTATTGCCAGGCTGGAGTGCATGGCATGAT 9120
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QY 9121 CTCGGCTCACTGTAACTCTCGCTCCAGGTTCAAGGATTCCTCTCTGCTCAGCCTCCCA 9180
Db 9121 CTCGGCTCACTGTAACTCTCGCTCCAGGTTCAAGGATTCCTCTCTGCTCAGCCTCCCA 9180
QY 9181 AGTAGCTGGGATACAGCGGTGCACCCATGCGCGCTAATTTTGTATTTTAGTAGA 9240
Db 9181 AGTAGCTGGGATACAGCGGTGCACCCATGCGCGCTAATTTTGTATTTTAGTAGA 9240
QY 9241 GACAGGGTTTCAACCATGTTGGCCAGGCTGTGCTCGAACTCTCTCTGACCTCGTATCGCC 9300
Db 9241 GACAGGGTTTCAACCATGTTGGCCAGGCTGTGCTCGAACTCTCTCTGACCTCGTATCGCC 9300
QY 9301 TGCCTCGGCCCTCCAAAGTGTGAGATTACAGGTGTGAGCCACCCCTGCCAGCCGTCAA 9360
Db 9301 TGCCTCGGCCCTCCAAAGTGTGAGATTACAGGTGTGAGCCACCCCTGCCAGCCGTCAA 9360
QY 9361 AGAGTCTTAAAT 9420
Db 9361 AGAGTCTTAAAT 9420
QY 9421 GCTGCATAAATGTGTACAAAGCTTCTCTTGAAGGCGAGGTCTTCAAGGATACCATAT 9480
Db 9421 GCTGCATAAATGTGTACAAAGCTTCTCTTGAAGGCGAGGTCTTCAAGGATACCATAT 9480
QY 9481 ACAGCTCAGAGTGTCTTTTAGGCATTAATTTAGCAAGATATCTCATCTCTCTCT 9540
Db 9481 ACAGCTCAGAGTGTCTTTTAGGCATTAATTTAGCAAGATATCTCATCTCTCTCT 9540
QY 9541 TTAACACCATTTCTTTTTTTTGTGTTAGAAAAGTATCTAGAAAAAGTAAATCTGATTT 9600
Db 9541 TTAACACCATTTCTTTTTTTTGTGTTAGAAAAGTATCTAGAAAAAGTAAATCTGATTT 9600
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Db 9601 ACCTCATTCTAGAAAGCTATAAAATGAATACAAATTAAGCTGTATTATTAATTAGCCAG 9660
QY 9661 TGAATAACTATTAAACACTTGTCTATTACCTGTGTAGTATTATTGTGCAATTAATAATGCA 9720
Db 9661 TGAATAACTATTAAACACTTGTCTATTACCTGTGTAGTATTATTGTGCAATTAATAATGCA 9720
QY 9721 TATACATTTAATAATGTATATGTATTGTATCTGATCATGATTTATGAAGTTCGTGTTC 9780
Db 9721 TATACATTTAATAATGTATATGTATTGTATCTGATCATGATTTATGAAGTTCGTGTTC 9780
QY 9781 ATCTTGATATATACATTAATCGCTTGTCTATTTTGGAGACATTTATTTTGCCTCTAAATTT 9840
Db 9781 ATCTTGATATATACATTAATCGCTTGTCTATTTTGGAGACATTTATTTTGCCTCTAAATTT 9840
QY 9841 CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGTAGCGGAATTAATCGTGT 9900
Db 9841 CTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGTAGCGGAATTAATCGTGT 9900
QY 9901 TCTTCACTCTAGGACATTTGCTCTAAGTTTGAAGACATTTGTTTATTACCGACAAC 9960
Db 9901 TCTTCACTCTAGGACATTTGCTCTAAGTTTGAAGACATTTGTTTATTACCGACAAC 9960
QY 9961 CATTCGAAGCATATGACAAATTAATTTCTCTCTTAATATCTTACTATCTGAAAGCAGA 10020
Db 9961 CATTCGAAGCATATGACAAATTAATTTCTCTCTTAATATCTTACTATCTGAAAGCAGA 10020
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Db 10021 CTGCTATAGGCTTCACTTACTCTCTACCTCATAGGAATATGTACAATTAATTTATT 10080
QY 10081 AGSTAAGCATTTGTTTTATATTGGTTTTATTTCACTGGCTGAGATTTCAAGAACACC 10140
Db 10081 AGSTAAGCATTTGTTTTATATTGGTTTTATTTCACTGGCTGAGATTTCAAGAACACC 10140
QY 10141 CGAGTCTTCACAGTAACACATTTCACTAACACATTTACTAACATCAGCAACTGTGGCT 10200
Db 10141 CGAGTCTTCACAGTAACACATTTCACTAACACATTTACTAACATCAGCAACTGTGGCT 10200
QY 10201 GTTAATTTTTTAATAGAAATTTAAGTCCCTCATTTTCTTCGGTGTATTTTAAGCTTAA 10260
Db 10201 GTTAATTTTTTAATAGAAATTTAAGTCCCTCATTTTCTTCGGTGTATTTTAAGCTTAA 10260
QY 10261 TTTTCTGGCTTTATTCATAAATCTTAAGGTCAACTACATTTGAAAAATCAAGACCTG 10320
Db 10261 TTTTCTGGCTTTATTCATAAATCTTAAGGTCAACTACATTTGAAAAATCAAGACCTG 10320
QY 10321 CATTTTAAATCTTATTCACCTCTGGCAAAACCAATTCACAAACCATGTTAGTAAAGAA 10380
Db 10321 CATTTTAAATCTTATTCACCTCTGGCAAAACCAATTCACAAACCATGTTAGTAAAGAA 10380
QY 10381 GGGTCACACCTGGTGGCCATAGGTAATGTACCAGGTGGTCCGGTGACAGAGATGCG 10440
Db 10381 GGGTCACACCTGGTGGCCATAGGTAATGTACCAGGTGGTCCGGTGACAGAGATGCG 10440
QY 10441 CGCTGAGGTTTTCTGAGGTAAAGGAATAAAGATGGGTGGAGGGCGTGCACCTGAA 10500
Db 10441 CGCTGAGGTTTTCTGAGGTAAAGGAATAAAGATGGGTGGAGGGCGTGCACCTGAA 10500
QY 10501 ATCATTGTAGAGAAACCCCTGAAATTTGAGAAACAAACAAAGAACTTACTTACCAG 10560
Db 10501 ATCATTGTAGAGAAACCCCTGAAATTTGAGAAACAAACAAAGAACTTACTTACCAG 10560
QY 10561 CTATTTGAATTTGCTGGAATACAGGCCATTCCTGAGCTGCTGAATGGGNACACACAG 10620
Db 10561 CTATTTGAATTTGCTGGAATACAGGCCATTCCTGAGCTGCTGAATGGGNACACACAG 10620
QY 10621 AAGGAAACAAACCACTCTGATAATCAITTTAGTCAAGTACAGCAGGTGATTGAGACTGC 10680
Db 10621 AAGGAAACAAACCACTCTGATAATCAITTTAGTCAAGTACAGCAGGTGATTGAGACTGC 10680
QY 10681 TGAGAGGTACAGGCCAAATTTCTTATGTTGTATTATTAATATGTCATCTTATAATCTGT 10740
Db 10681 TGAGAGGTACAGGCCAAATTTCTTATGTTGTATTATTAATATGTCATCTTATAATCTGT 10740

QY 10741 CAGTATTTTATAAAACATTTCTTCAAAACTCACACATTTAAAAACAACACACTGTCTC 10800
Db 10741 CAGTATTTTATAAAACATTTCTTCAAAACTCACACATTTAAAAACAACACACTGTCTC 10800
QY 10801 TAAATCCCAAAATTTTTCATAAAC 10825
Db 10801 TAAATCCCAAAATTTTTCATAAAC 10825
RESULT 6
LOCUS ARL149460 10825 bp DNA linear PAT 08-AUG-2001
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ACCESSION ARL149460
VERSION ARL149460.1 GI:15114051
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas, W. J., Drayna, D. T., Feder, J. N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z., and Wolff, R. K.
TITLE Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
JOURNAL Patent: US 6228594-A 3 08-MAY-2001;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 10823; DB 6; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTAAGTTTGAGATATAAATTTTAAATGTATGATTGAATTTGAAATATCAATAATATTTA 60
Db 1 TCTAAGTTTGAGATATAAATTTTAAATGTATGATTGAATTTGAAATATCAATAATATTTA 60
QY 61 AATATCTAAAGTTTCAGATCAGACATTCGAAAGTACTTTCCCAATCAACAACACCCCT 120
Db 61 AATATCTAAAGTTTCAGATCAGACATTCGAAAGTACTTTCCCAATCAACAACACCCCT 120
QY 121 TCAGGATTTAAAAACCAAGGGGACACTGATCACCCTAGTGTTCACAGCAGGTACCTT 180
Db 121 TCAGGATTTAAAAACCAAGGGGACACTGATCACCCTAGTGTTCACAGCAGGTACCTT 180
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCCACGAGGAATT 240
Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCCACGAGGAATT 240
QY 241 TTACTGGCATCTCTCAGCCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCG 300
Db 241 TTACTGGCATCTCTCAGCCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCG 300
QY 301 TTTCCCGCCCCCAAAAGACGGAGATTTAACGGGACGTGCGGCCAGAGCTGGGAA 360
Db 301 TTTCCCGCCCCCAAAAGACGGAGATTTAACGGGACGTGCGGCCAGAGCTGGGAA 360
QY 361 ATGGGCGCGGAGCCAGCGCGGCTTCTCCTCTGATGCTTTTGCAGACCCGGTCTTG 420
Db 361 ATGGGCGCGGAGCCAGCGCGGCTTCTCCTCTGATGCTTTTGCAGACCCGGTCTTG 420
QY 421 CAGGGCGCTTGTGCTGAGTCCGAGGGCTCGGGCCGAACCTAGGGCCGCGGGGGTG 480
Db 421 CAGGGCGCTTGTGCTGAGTCCGAGGGCTCGGGCCGAACCTAGGGCCGCGGGGGTG 480
QY 481 GAAAAATCGAAACTAGCTTTTCTTTTGGCCTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540
Db 481 GAAAAATCGAAACTAGCTTTTCTTTTGGCCTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540

[illegible]

Qy	3841	CGTGGATGACCACGCTGTTGCTGTTCTATGATNATGAGAGTGCCTGTGTGGAGCCCCGAAC	3900
Db	3841	CGTGGATGACCACGCTGTTGCTGTTCTATGATCATGAGAGTGCCTGTGTGGAGCCCCGAAC	3900
Qy	3901	TCCATGGGTTTCCACGTAGAAATTCAAAGCCAGATGTGGCTGCAGCTGAGTCAAGACTCTGAA	3960
Db	3901	TCCATGGGTTTCCAGTGTAGAAATTCAAAGCCAGATGTGGCTGCAGCTGAGTCAAGACTCTGAA	3960
Qy	3961	AGGTTGGGATACATGTTCACTGTTGACTTCTGGAATATTTATGGAATATCACACACACAC	4020
Db	3961	AGGTTGGGATACATGTTCACTGTTGACTTCTGGAATATTTATGGAATATCACACACACAC	4020
Qy	4021	CAAGGGTATGTGGAGAGGGGGCCTACCTTCTCGAGGTTGTCAAGAGCTTTTCATCTTTTC	4080
Db	4021	CAAGGGTATGTGGAGAGGGGGCCTACCTTCTCGAGGTTGTCAAGAGCTTTTCATCTTTTC	4080
Qy	4081	ATGCATCTTGAAGGAACACGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGGAAGAGGAAG	4140
Db	4081	ATGCATCTTGAAGGAACACGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGGAAGAGGAAG	4140
Qy	4141	GAATTTGCTCTCTGAGATCATTTGTTGCTTGGGGATGTGGAAATATGGAACCTATTCTT	4200
Db	4141	GAATTTGCTCTCTGAGATCATTTGTTGCTTGGGGATGTGGAAATATGGAACCTATTCTT	4200
Qy	4201	TGSGTTCAGATTACAGAGCTGGGGATTTTTCAGAGTCCCACACCTCCAGGTCACTCTG	4260
Db	4201	TGSGTTCAGATTACAGAGCTGGGGATTTTTCAGAGTCCCACACCTCCAGGTCACTCTG	4260
Qy	4261	GGCTGTGAAATGCAAGAGAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
Db	4261	GGCTGTGAAATGCAAGAGAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
Qy	4321	CAGGACCACTTCAATTTCTGCCCTGACACACTGGATTTGGAGAGCAGACAACCCAGGGCC	4380
Db	4321	CAGGACCACTTGAATTTCTGCCCTGACACACTGGATTTGGAGAGCAGACAACCCAGGGCC	4380
Qy	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGATTCGGGGCCAGCGACAACAGGGCCCTAC	4440
Db	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGATTCGGGGCCAGCGACAACAGGGCCCTAC	4440
Qy	4441	CTGGAGAGGACTTCGCCCTGCACAGCTGCAGCAGTTGCTGAGAGTGGCTGGAGAGGTGTTTG	4500
Db	4441	CTGGAGAGGACTTCGCCCTGCACAGCTGCAGCAGTTGCTGAGAGTGGCTGGAGAGGTGTTTG	4500
Qy	4501	GACCAACAAGGTATGTGTGGAACACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG	4560
Db	4501	GACCAACAAGGTATGTGTGGAACACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG	4560
Qy	4561	AGGTTGAGGGCAGCGAATCCCTGGTGTGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCCTC	4620
Db	4561	AGGTTGAGGGCAGCGAATCCCTGGTGTGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCCTC	4620
Qy	4621	TCCAAATTTCTGGGAAGGACTTTTCAATCTCTAGTCTCTACCTTTAATTTAGAGTGA	4680
Db	4621	TCCAAATTTCTGGGAAGGACTTTTCAATCTCTAGTCTCTACCTTTAATTTAGAGTGA	4680
Qy	4681	TGAGACGCCACAAGTCAATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAAGGAA	4740
Db	4681	TGAGACGCCACAAGTCAATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAAGGAA	4740
Qy	4741	GTGTCTATGGCCCTTGCTTTTATTTAAACAATAATCTTTTGATATTTATACCTGTTAA	4800
Db	4741	GTGTCTATGGCCCTTGCTTTTATTTAAACAATAATCTTTTGATATTTATACCTGTTAA	4800
Qy	4801	AAATTCAGAAATGTCAAGCGCGGACGGTGCACCCCTGTAATCCACGACCTTTGGG	4860
Db	4801	AAATTCAGAAATGTCAAGCGCGGACGGTGCACCCCTGTAATCCACGACCTTTGGG	4860
Qy	4861	AGGCCGAGCGGGGTGGTCAACAAGTCAAGAGTTGAGACAGCCCTGACCAACATGGTGAA	4920
Db	4861	AGGCCGAGCGGGGTGGTCAACAAGTCAAGAGTTGAGACAGCCCTGACCAACATGGTGAA	4920

QY	4921	ACCCGTC	TCTAAAAA	TACAAAAA	TTAGTGGT	CACAGT	CAATGG	CACACCT	TAGTCCCA	4980
Db	4921	ACCCGTC	TCTAAAAA	TACAAAAA	TTAGTGGT	CACAGT	CAATGG	CACACCT	TAGTCCCA	4980
QY	4981	GCTAAT	TGGAAGG	CTGAGG	CAGGACAT	CCGTTG	CAACCT	TGGGAAG	CGGAAGTTGCAC	TGA 5040
Db	4981	GCTAAT	TGGAAGG	CTGAGG	CAGGACAT	CCGTTG	CAACCT	TGGGAAG	CGGAAGTTGCAC	TGA 5040
QY	5041	GCCAA	GATCGCG	CCACTGC	ACTCCAG	CGCTAGG	CAGCAG	AGAGT	GAGATCC	ATCTTAAAAA 5100
Db	5041	GCCAA	GATCGCG	CCACTGC	ACTCCAG	CGCTAGG	CAGCAG	AGAGT	GAGATCC	ATCTTAAAAA 5100
QY	5101	AAAAA	AAAAA	AAAAA	GAGAA	TTACAG	ATCTC	AGCTAT	CATATCA	ATAACACGACAAA 5160
Db	5101	AAAAA	AAAAA	AAAAA	GAGAA	TTACAG	ATCTC	AGCTAT	CATATCA	ATAACACGACAAA 5160
QY	5161	ATATC	AAGTGAGG	CCACTT	ATCAG	AGTAA	GAAATCC	TTTAGT	GTAAAAA	TTTCTTTTCAT 5220
Db	5161	ATATC	AAGTGAGG	CCACTT	ATCAG	AGTAA	GAAATCC	TTTAGT	GTAAAAA	TTTCTTTTCAT 5220
QY	5221	AGAAC	ATAGCA	ATAAT	CTACTG	AACTAC	CTTAC	AGTCCG	CTTCTTT	TATAACAAATGC 5280
Db	5221	AGAAC	ATAGCA	ATAAT	CTACTG	AACTAC	CTTAC	AGTCCG	CTTCTTT	TATAACAAATGC 5280
QY	5281	CTCCT	AGGTTG	ACCCAG	GTGAA	ACTGAC	ATCTCT	ATTTC	CAATCAT	TTTCAATGCACATAA 5340
Db	5281	CTCCT	AGGTTG	ACCCAG	GTGAA	ACTGAC	ATCTCT	ATTTC	CAATCAT	TTTCAATGCACATAA 5340
QY	5341	AGGCA	AAATTT	TATCT	ATCAG	AAACAA	AGGTA	AGGTAC	AGATAT	GTATATTTACATGTG 5400
Db	5341	AGGCA	AAATTT	TATCT	ATCAG	AAACAA	AGGTA	AGGTAC	AGATAT	GTATATTTACATGTG 5400
QY	5401	AGCAG	AACAG	CTGATC	GTACTG	CTCTC	CAAGT	GACACT	GTGTAG	AGTCCCAATCTTAGG 5460
Db	5401	AGCAG	AACAG	CTGATC	GTACTG	CTCTC	CAAGT	GACACT	GTGTAG	AGTCCCAATCTTAGG 5460
QY	5461	ACACA	AAATGG	TCTCT	CTCTCT	CTAG	CTGTG	TTTTT	CTGAAA	AGGGTATTTCTCTCTCTC 5520
Db	5461	ACACA	AAATGG	TCTCT	CTCTCT	CTAG	CTGTG	TTTTT	CTGAAA	AGGGTATTTCTCTCTCTC 5520
QY	5521	AACT	ATAGAA	GAGTGA	AGACTT	CCAGT	CTTCT	CTGGCA	AGGGTAA	ACAGATCCCCTCTC 5580
Db	5521	AACT	ATAGAA	GAGTGA	AGACTT	CCAGT	CTTCT	CTGGCA	AGGGTAA	ACAGATCCCCTCTC 5580
QY	5581	CTCAT	CTCTCT	CTCTCT	CTCA	AGTG	CGCTCT	CTTTG	GTGA	AGGTGACACATCATGTGACC 5640
Db	5581	CTCAT	CTCTCT	CTCTCT	CTCA	AGTG	CGCTCT	CTTTG	GTGA	AGGTGACACATCATGTGACC 5640
QY	5641	TC	TCAGT	GACCA	CTCTAC	GGTGTG	GGCCTG	GA	CTACTAC	CCCCCAGAACATCACCATTG 5700
Db	5641	TC	TCAGT	GACCA	CTCTAC	GGTGTG	GGCCTG	GA	CTACTAC	CCCCCAGAACATCACCATTG 5700
QY	5701	AA	GTGGCT	GAA	GGAATA	AGCAG	CCAAT	TGGATG	CCAA	GAGGTTGCGAACCTTAAGACGTATTG 5760
Db	5701	AA	GTGGCT	GAA	GGAATA	AGCAG	CCAAT	TGGATG	CCAA	GAGGTTGCGAACCTTAAGACGTATTG 5760
QY	5761	CCCA	ATGGG	GATGG	GACCTT	ACAGG	CGCTGG	ATAA	CCCTT	GGCTGTACCCCTGGGGAAGAG 5820
Db	5761	CCCA	ATGGG	GATGG	GACCTT	ACAGG	CGCTGG	ATAA	CCCTT	GGCTGTACCCCTGGGGAAGAG 5820
QY	5821	CAG	ATATAC	GTNCCA	AGTGTG	GAGCACC	CAGG	CCCTGG	ATCAG	CCCCCTCATTTGTGATCTGG 5880
Db	5821	CAG	ATATAC	GTNCCA	AGTGTG	GAGCACC	CAGG	CCCTGG	ATCAG	CCCCCTCATTTGTGATCTGG 5880
QY	5881	GGT	ATGT	ACTG	ATG	AGAG	CCAGG	ACTG	AGAAA	TCTATTGGGGGGTTGAGAGAGTGGC 5940
Db	5881	GGT	ATGT	ACTG	ATG	AGAG	CCAGG	ACTG	AGAAA	TCTATTGGGGGGTTGAGAGAGTGGC 5940
QY	5941	TG	AGAG	GTAA	TAT	TGCA	CTG	AGAT	GTCT	CTTTTGTAGGGGGTGGGCTGAGG 6000
Db	5941	TG	AGAG	GTAA	TAT	TGCA	CTG	AGAT	GTCT	CTTTTGTAGGGGGTGGGCTGAGG 6000
QY	6001	GTG	GCAAT	CAAA	GCGTTT	TAAT	CTG	TTTTT	TAG	AGCCCTTACCGTCTGGCACCC 6060

Db	6001	GTGGCAATCAAAAGGCTTTAACTGCTTTTCTGTTTTAGAGCCCTCACGCTCTGGCACCC	6060
Qy	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTGTGTCATCTGTTGTCATTGGAAATTT	6120
Db	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTGTGTCATCTGTTGTCATTGGAAATTT	6120
Qy	6121	TGTTCAATAATATTAGGAAGAGGACGGGTCAAGTGAGTAGGAAACAGGGGGAAGTCTCT	6180
Db	6121	TGTTCAATAATATTAGGAAGAGGACGGGTCAAGTGAGTAGGAAACAGGGGGAAGTCTCT	6180
Qy	6181	TAGTACTCTGCCCAAGGACAGTGGGAAGAGGGGACAGAGGGGATCTGGCATCCATGGG	6240
Db	6181	TAGTACTCTGCCCAAGGACAGTGGGAAGAGGGGACAGAGGGGATCTGGCATCCATGGG	6240
Qy	6241	AAGCAPTTTTCTCATTTATATATCTTTTGGGGACACAGCAGCTCCTTGGGAGACAGAAAT	6300
Db	6241	AAGCAPTTTTCTCATTTATATCTTTTGGGGACACAGCAGCTCCTTGGGAGACAGAAAT	6300
Qy	6301	AATGGTCTCCCCCAAGTGAAGTCTCTAAATTCAACAACAATCTTCAGAGCACTACTAT	6360
Db	6301	AATGGTCTCCCCCAAGTGAAGTCTCTAAATTCAACAACAATCTTCAGAGCACTACTAT	6360
Qy	6361	TTTTCGAAGAGCTGTTTAAAGTGTAGTACAGGGCTTTGAGTTTGAAAGTCTACTGTGGGTAT	6420
Db	6361	TTTTCGAAGAGCTGTTTAAAGTGTAGTACAGGGCTTTGAGTTTGAAAGTCTACTGTGGGTAT	6420
Qy	6421	TCACGAACCCAAATCTGCTAGGGAATGAAATGTATACAGTAAGTAAATCTAGTTAAAGAAG	6480
Db	6421	TCACGAACCCAAATCTGCTAGGGAATGAAATGTATACAGTAAGTAAATCTAGTTAAAGAAG	6480
Qy	6481	ACCCCATGAGGTCCTTAAAGCAGGCAGGAAGCAAAATGCTTTAGGGTGTCAAAGGAAAGAATG	6540
Db	6481	ACCCCATGAGGTCCTTAAAGCAGGCAGGAAGCAAAATGCTTTAGGGTGTCAAAGGAAAGAATG	6540
Qy	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGATCTTGAAGGAGAGCTGATTTCCA	6600
Db	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGATCTTGAAGGAGAGCTGATTTCCA	6600
Qy	6601	TTAGGTGAGGTTCAAGATGATGGAGGCTCACACAGAGGGAGCAACCATGCCAAGTAGGA	6660
Db	6601	TTAGGTGAGGTTCAAGATGATGGAGGCTCACACAGAGGGAGCAACCATGCCAAGTAGGA	6660
Qy	6661	GAGTATAAGGCATCTCTGGGAGATTAGAAATAATTACTGTACCTTAAACCTGANGTTGGGT	6720
Db	6661	GAGTATAAGGCATCTCTGGGAGATTAGAAATAATTACTGTACCTTAAACCTGANGTTGGGT	6720
Qy	6721	AGCTATCACTTACCAATATTGCAATTTCTACCCCTGAACATCTGTGGTGTAGGGAANAAGA	6780
Db	6721	AGCTATCACTTACCAATATTGCAATTTCTACCCCTGAACATCTGTGGTGTAGGGAANAAGA	6780
Qy	6781	GAATCAGAAAGAACCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA	6840
Db	6781	GAATCAGAAAGAACCCAGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTTATGA	6840
Qy	6841	TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGCCAGATCTCCCTTATATGGTG	6900
Db	6841	TCACTGGGGTGTCATTGAAGGATCCTAAGAAAGGAGGCCAGATCTCCCTTATATGGTG	6900
Qy	6901	AATGTTGTTTAAAGATTAGATGAGAGTGTAGGAGACACCAAGTTAGAAAGCCCAATAAGCAT	6960
Db	6901	AATGTTGTTTAAAGATTAGATGAGAGTGTAGGAGACACCAAGTTAGAAAGCCCAATAAGCAT	6960
Qy	6961	TTCCAGATGAGAGATAATGGTTCTTGAAATCCCAATAGTGCCCAAGTCTAAATTTAGATGG	7020
Db	6961	TTCCAGATGAGAGATAATGGTTCTTGAAATCCCAATAGTGCCCAAGTCTAAATTTAGATGG	7020
Qy	7021	GTGAATGAGGAAAATAGGAGACAGAGAGCAAGATGGTGCTAGGTTTCTGTGATGCCT	7080
Db	7021	GTGAATGAGGAAAATAGGAGAGAGAGAGCAAGATGGTGCTAGGTTTCTGTGATGCCT	7080
Qy	7081	CTTTTCTCTGGGTCTCTGTCTCCACAGGAGGAGCCATGGGSCACTACGTTTACGTGAACG	7140

Db 7081 CTTTCTGGGTCTCTTGTCTCCACAGGAGGCCATGGGCACACTACGTTCTTAGCTGAACG 7140
QY 7141 TGAGTGACACGAGCCTGCAGACTCACTCTGGGAGGAGACAAAACACTAGACACTCAAGA 7200
Db 7141 TGAGTGACACGAGCCTGCAGACTCACTCTGGGAGGAGACAAAACACTAGACACTCAAGA 7200
QY 7201 GGGAGTGCATTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT 7260
Db 7201 GGGAGTGCATTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT 7260
QY 7261 GCCTGACGAACCTCCTGATTTAGCCTCTCTGTTTCATTTCTCATAAAGATTTCCCAT 7320
Db 7261 GCCTGACGAACCTCCTGATTTAGCCTCTCTGTTTCATTTCTCATAAAGATTTCCCAT 7320
QY 7321 TTAGGTTTCTGAGTTCCCTGCATGCCGTTGATCCCTAGCTGTGACCTCTCCCTGSAAC 7380
Db 7321 TTAGGTTTCTGAGTTCCCTGCATGCCGTTGATCCCTAGCTGTGACCTCTCCCTGSAAC 7380
QY 7381 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCATTTCTCCTCGTCAACCTCAGAG 7440
Db 7381 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCATTTCTCCTCGTCAACCTCAGAG 7440
QY 7441 ACATACACCTATGTCATTTTCATTTTCCATTTTGGAGAGGACTCCTTAAATTTGGGGGA 7500
Db 7441 ACATACACCTATGTCATTTTCATTTTCCATTTTGGAGAGGACTCCTTAAATTTGGGGGA 7500
QY 7501 CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCTGGGAGCTGGCTAGTCA 7560
Db 7501 CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCTGGGAGCTGGCTAGTCA 7560
QY 7561 AACCTTACAGATTTTACACATGATCTATGCAATTTCTGGACCCGTTCAACCTTTCC 7620
Db 7561 AACCTTACAGATTTTACACATGATCTATGCAATTTCTGGACCCGTTCAACCTTTCC 7620
QY 7621 TTGAATCTCTCTCTGTTTACCCAGTAACCTCATCTGTCACCAAGCCTTGGGGATTTTC 7680
Db 7621 TTGAATCTCTCTCTGTTTACCCAGTAACCTCATCTGTCACCAAGCCTTGGGGATTTTC 7680
QY 7681 CATCTGATGTGATGTAGTTGCAAGCTATGAAGCTGTACACTGCACGAATGCAAGAG 7740
Db 7681 CATCTGATGTGATGTAGTTGCAAGCTATGAAGCTGTACACTGCACGAATGCAAGAG 7740
QY 7741 GCACCTGTCACGAAAAAGCATCATGCTATCTGTTGGGTAGTATGATGGGTGTTTTAGC 7800
Db 7741 GCACCTGTCACGAAAAAGCATCATGCTATCTGTTGGGTAGTATGATGGGTGTTTTAGC 7800
QY 7801 AGGTAGGAGCAAAATATCTTCAAGGGGTGTTGAAGAGGTGTTTTCTTAATGGCATGA 7860
Db 7801 AGGTAGGAGCAAAATATCTTCAAGGGGTGTTGAAGAGGTGTTTTCTTAATGGCATGA 7860
QY 7861 AGGTGTCATACAGATTGCAAAAGTTTAAATGTCCTTCATTTGGGATGCTACTAGTAT 7920
Db 7861 AGGTGTCATACAGATTGCAAAAGTTTAAATGTCCTTCATTTGGGATGCTACTAGTAT 7920
QY 7921 TCCAGACCTGAAGATCAACAATAATTTCTACCTGGTCTCCCTGTTGTTCTGATAAAGAA 7980
Db 7921 TCCAGACCTGAAGATCAACAATAATTTCTACCTGGTCTCCCTGTTGTTCTGATAAAGAA 7980
QY 7981 ATTATGATAAGGATGATAAAGCACTTACTTCGTGTCGGACTCTTCTGAGCACCTACTTA 8040
Db 7981 ATTATGATAAGGATGATAAAGCACTTACTTCGTGTCGGACTCTTCTGAGCACCTACTTA 8040
QY 8041 CATGCATTACTGCATGCACTTCTTACAAATATTTCTATGATAGATGTTACTATATCCCAT 8100
Db 8041 CATGCATTACTGCATGCACTTCTTACAAATATTTCTATGATAGATGTTACTATATCCCAT 8100
QY 8101 TTTCTTTTAAATGAAGAAAGTAGGCGGGCAGGCTGGCTCAGCCTGTATATCC 8160
Db 8101 TTTCTTTTAAATGAAGAAAGTAGGCGGGCAGGCTGGCTCAGCCTGTATATCC 8160
QY 8161 AGCACTTTGGAGGCCAAAGCGGTGGATCAGAGGTCAGAGATCGAGACCATCTGGC 8220
Db 8161 AGCACTTTGGAGGCCAAAGCGGTGGATCAGAGGTCAGAGATCGAGACCATCTGGC 8220

QY 8221 TAACATGGTGAACCCCATCTCTAATAAAAAATACAAAAAATTAGCTGGCGTGGTGCAG 8280
Db 8221 TAACATGGTGAACCCCATCTCTAATAAAAAATACAAAAAATTAGCTGGCGTGGTGCAG 8280
QY 8281 ACGCCTCTAGTCCAGCTACTCGGAAGGCTGAGCAGGAGAAATGGCATGAACCCAGGAG 8340
Db 8281 ACGCCTCTAGTCCAGCTACTCGGAAGGCTGAGCAGGAGAAATGGCATGAACCCAGGAG 8340
QY 8341 CAGAGCTTGCAGTGAAGCCAGTTTGGCCCACTGCACCTCCAGCCTAGGTGACAGAGTGAGA 8400
Db 8341 CAGAGCTTGCAGTGAAGCCAGTTTGGCCCACTGCACCTCCAGCCTAGGTGACAGAGTGAGA 8400
QY 8401 CTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 8460
Db 8401 CTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 8460
QY 8461 TAGAGTATCTCATAGTTTGTCACTGATAGAAACAGAGTTTCAAACTCAGTCAATCTCACCG 8520
Db 8461 TAGAGTATCTCATAGTTTGTCACTGATAGAAACAGAGTTTCAAACTCAGTCAATCTCACCG 8520
QY 8521 TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCTTAGATTAATAGAGAA 8580
Db 8521 TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCTTAGATTAATAGAGAA 8580
QY 8581 GGAAGGAGATGGCTCTCTCTCTCATTTGTTCTTCTGAGTGAGCTTGAATCACAT 8640
Db 8581 GGAAGGAGATGGCTCTCTCTCTCATTTGTTCTTCTGAGTGAGCTTGAATCACAT 8640
QY 8641 GAAGGGGAACAGAGAAAAACAACAACTGATCCTCAGCTGTCTATGTTTCTTTAAAGTC 8700
Db 8641 GAAGGGGAACAGAGAAAAACAACAACTGATCCTCAGCTGTCTATGTTTCTTTAAAGTC 8700
QY 8701 CCTGAAGGAAGTCTTGGAAATGTAATGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8760
Db 8701 CCTGAAGGAAGTCTTGGAAATGTAATGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8760
QY 8761 TTTCTTTGGACCCCTACGCAAGGACTGTAATGTTGGTGGGACAGCTAGTGCCCTGCTGGC 8820
Db 8761 TTTCTTTGGACCCCTACGCAAGGACTGTAATGTTGGTGGGACAGCTAGTGCCCTGCTGGC 8820
QY 8821 TTCACACAGCTGTCCTCCTAGGCCAGTGCCTCTCGAGTCAGAACTCTGGTGGTATTC 8880
Db 8821 TTCACACAGCTGTCCTCCTAGGCCAGTGCCTCTCGAGTCAGAACTCTGGTGGTATTC 8880
QY 8881 CCTCAATGAAGTGAGTAAAGCTCTCTCAATTTGAGATGTAATAATGGAAGCCACCAAGTG 8940
Db 8881 CCTCAATGAAGTGAGTAAAGCTCTCTCAATTTGAGATGTAATAATGGAAGCCACCAAGTG 8940
QY 8941 GCTTAGAGGATGCCAGGTCCTTCCATGGAGCAGCTGGGGTTCCGGTGACACATTAATAA 9000
Db 8941 GCTTAGAGGATGCCAGGTCCTTCCATGGAGCAGCTGGGGTTCCGGTGACACATTAATAA 9000
QY 9001 AATACTAACAGGACATTCAGGAATTCAGATTCGGAATAATCAGTTCACCATGTTCA 9060
Db 9001 AATACTAACAGGACATTCAGGAATTCAGATTCGGAATAATCAGTTCACCATGTTCA 9060
QY 9061 AAAGAGTCTTT 9120
Db 9061 AAAGAGTCTTT 9120
QY 9121 CTCGGCTCACTGTAACCTCTGCCCTCCAGGTTCAAGCGATTCCTCTGTCTCAGCCTCCCA 9180
Db 9121 CTCGGCTCACTGTAACCTCTGCCCTCCAGGTTCAAGCGATTCCTCTGTCTCAGCCTCCCA 9180
QY 9181 AGTAGCTGGATACAGGCGTGCACCAACCATGCCGGCTAAATTTTGTATTTTTAGTAGA 9240
Db 9181 AGTAGCTGGATACAGGCGTGCACCAACCATGCCGGCTAAATTTTGTATTTTTAGTAGA 9240
QY 9241 GACAGGTTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCTGACCTCGTATCCGCC 9300
Db 9241 GACAGGTTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCTGACCTCGTATCCGCC 9300

Qy	9301	TG	CC	TCCGGCCTCCCAAGT	GCTGAGAT	TACAG	TGTGAGCCACCCCTG	CCCGACGGT	CACA	9360		
Db	9301	TG	CC	TCCGGCCTCCCAAGT	GCTGAGAT	TACAG	TGTGAGCCACCCCTG	CCCGACGGT	CACA	9360		
Qy	9361	AG	AG	CTTTAAATATATAT	ATATCC	AGATGG	CGATGTGTTACT	TATGTTACT	ACATGCACTTG	9420		
Db	9361	AG	AG	CTTTAAATATATAT	ATATCC	AGATGG	CGATGTGTTACT	TATGTTACT	ACATGCACTTG	9420		
Qy	9421	G	CT	GCATAAATG	TGGTAC	AAGCA	ATCTGCTG	GAAGGCGAGG	TGCTTCAGGATAC	9480		
Db	9421	G	CT	GCATAAATG	TGGTAC	AAGCA	ATCTGCTG	GAAGGCGAGG	TGCTTCAGGATAC	9480		
Qy	9481	AC	AG	CTCAGAGT	TTCTCT	TTTAGG	CGATAAATTTT	TAGCAAGAGAT	ATCTCATCTCTCTT	9540		
Db	9481	AC	AG	CTCAGAGT	TTCTCT	TTTAGG	CGATAAATTTT	TAGCAAGAGAT	ATCTCATCTCTCTT	9540		
Qy	9541	TT	AA	CAACATTTCT	TTTTTT	TGTGGT	TAGAAAGTTAT	TGTAGAAAAAG	TAAATGTGATTT	9600		
Db	9541	TT	AA	CAACATTTCT	TTTTTT	TGTGGT	TAGAAAGTTAT	TGTAGAAAAAG	TAAATGTGATTT	9600		
Qy	9601	AC	GC	TCATTTAG	AAAAAGCT	ATAA	ANTGA	TACAAATTTAA	AGCTGTATTTAA	TAGCCAG	9660	
Db	9601	AC	GC	TCATTTAG	AAAAAGCT	ATAA	ANTGA	TACAAATTTAA	AGCTGTATTTAA	TAGCCAG	9660	
Qy	9661	T	G	AAAACTATTA	CAACCT	GTCTAT	TACCTGT	TAGTATTTAT	TGTCGCA	TAAAAATGCA	9720	
Db	9661	T	G	AAAACTATTA	CAACCT	GTCTAT	TACCTGT	TAGTATTTAT	TGTCGCA	TAAAAATGCA	9720	
Qy	9721	T	A	TACTTTAA	ATGATAT	TGTA	TGTAT	TAC	TGCA	TGATTTTAT	TGAGAGTCTG	9780
Db	9721	T	A	TACTTTAA	ATGATAT	TGTA	TGTAT	TAC	TGCA	TGATTTTAT	TGAGAGTCTG	9780
Qy	9781	A	T	CTTGCTAT	ATACTTA	ATCGCT	TTGTCAT	TTTGGAGACAT	TTTATTTGCT	CTCTAAATTT	9840	
Db	9781	A	T	CTTGCTAT	ATACTTA	ATCGCT	TTGTCAT	TTTGGAGACAT	TTTATTTGCT	CTCTAAATTT	9840	
Qy	9841	C	T	TACATTTT	TGCTTT	ACGGA	ATATTTT	CA	TTCAC	TGTGGTAGCCGAA	TATATTCG	9900
Db	9841	C	T	TACATTTT	TGCTTT	ACGGA	ATATTTT	CA	TTCAC	TGTGGTAGCCGAA	TATATTCG	9900
Qy	9901	T	C	TCACCT	CTAGG	GACAT	TGCGT	CTA	AGTGT	TAGACAT	TGTTATTT	9960
Db	9901	T	C	TCACCT	CTAGG	GACAT	TGCGT	CTA	AGTGT	TAGACAT	TGTTATTT	9960
Qy	9961	C	A	TCTGAA	AGCATAT	GACAA	ATTTT	TCT	CTCT	TAAAT	TCTTACT	10020
Db	9961	C	A	TCTGAA	AGCATAT	GACAA	ATTTT	TCT	CTCT	TAAAT	TCTTACT	10020
Qy	10021	C	T	GCTTAA	AGGCTTC	ACCTT	ACTCT	TAC	CTC	AT	AAGGA	10080
Db	10021	C	T	GCTTAA	AGGCTTC	ACCTT	ACTCT	TAC	CTC	AT	AAGGA	10080
Qy	10081	A	G	TTAAG	CAATTTG	TTTAT	TGTTT	TATTT	TTCAC	CTGGCT	GAGATTT	10140
Db	10081	A	G	TTAAG	CAATTTG	TTTAT	TGTTT	TATTT	TTCAC	CTGGCT	GAGATTT	10140
Qy	10141	C	A	GCTT	CTCAG	GTAA	ACATTT	CT	CA	TAA	CA	10200
Db	10141	C	A	GCTT	CTCAG	GTAA	ACATTT	CT	CA	TAA	CA	10200
Qy	10201	G	T	TAA	TTTTTTT	TA	TAGAA	TTTTT	TAA	GCTC	CA	10260
Db	10201	G	T	TAA	TTTTTTT	TA	TAGAA	TTTTT	TAA	GCTC	CA	10260
Qy	10261	T	T	TCT	TGCTTT	TAT	TCATA	AAATCT	T	T	AAGG	10320
Db	10261	T	T	TCT	TGCTTT	TAT	TCATA	AAATCT	T	T	AAGG	10320
Qy	10321	C	A	TTTT	TAAAT	CTT	TAT	CAC	CT	TG	CA	10380
Db	10321	C	A	TTTT	TAAAT	CTT	TAT	CAC	CT	TG	CA	10380
Qy	10381	G	G	T	G	T	C	A	C	T	G	10440

Db	10381	GGGTACACCTGGTGGCCATAGGTAATGTACCACGGTGGTCCGGTGACCAGATGCAG	10440
Qy	10441	CGCTGAGGGTTTTCTCTGAAAGTAAGGAATAAAGATGGGTGGAGGGCGGTGCACCTGGAA	10500
Db	10441	CGCTGAGGGTTTTCTCTGAAAGTAAGGAATAAAGATGGGTGGAGGGCGGTGCACCTGGAA	10500
Qy	10501	ATCACTTGTAGAGAAAAGCCCTCAAAATTTGAGAAAACAACAAGAAACACTTACTTTACCAG	10560
Db	10501	ATCACTTGTAGAGAAAAGCCCTCAAAATTTGAGAAAACAACAAGAAACACTTACTTTACCAG	10560
Qy	10561	CTATTGAAATTCGTGGAAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACAACAACAG	10620
Db	10561	CTATTGAAATTCGTGGAAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACAACAACAG	10620
Qy	10621	AAGGAAACAACAACACACTCTGATATCATTTGATGAGTCAAGTACAGCAGGTGATTGAGGACTGC	10680
Db	10621	AAGGAAACAACAACACACTCTGATATCATTTGATGAGTCAAGTACAGCAGGTGATTGAGGACTGC	10680
Qy	10681	TGAGAGGTACAGGCCAAAATTCCTTATGTTGATATATATATATATATATATATATATATATCTGT	10740
Db	10681	TGAGAGGTACAGGCCAAAATTCCTTATGTTGATATATATATATATATATATATATATATCTGT	10740
Qy	10741	CAGTATTTTATAAACAATCTTTCACAACTCACACACATTTAAAAACAACAACACTGTCTC	10800
Db	10741	CAGTATTTTATAAACAATCTTTCACAACTCACACACATTTAAAAACAACAACACTGTCTC	10800
Qy	10801	TAAATCCCAAAATTTTCATAAAC	10825
Db	10801	TAAATCCCAAAATTTTCATAAAC	10825
RESULT	7		
LOCUS	AR149461	10825 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 5 from patent US 6228594.		
ACCESSION	AR149461		
VERSION	AR149461.1	GI:15114052	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 10825)		
AUTHORS	Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.		
TITLE	Method for determining the presence or absence of a hereditary hemochromatosis gene mutation		
JOURNAL	Patent: US 6228594-A 5 08-MAY-2001;		
FEATURES	Location/Qualifiers		
source	1..10825		
BASE COUNT	2998 a 2252 c 2649 g	2926 t	
ORIGIN			
Query Match	100.0%;	Score 10823;	DB 6; Length 10825;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 10823;	Conservative 0;	Mismatches 2;	Indels 0; Gaps
Qy	1	TCTAAGGTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATAATCATATAATTTA	60
Db	1	TCTAAGGTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATAATCATATAATTTA	60
Qy	61	AATATCTAAAGTTCAGATCAGAACATTTGGGAAGCTACTTCCCAATCAACAACCCCT	120
Db	61	AATATCTAAAGTTCAGATCAGAACATTTGGGAAGCTACTTCCCAATCAACAACCCCT	120
Qy	121	TCAGAGTTTAAAAACAAGGGGACACTGGATCACCTAGTGTTCACAGCAGGTACCTT	180
Db	121	TCAGAGTTTAAAAACAAGGGGACACTGGATCACCTAGTGTTCACAGCAGGTACCTT	180
Qy	181	CTGCTGTAGGAGAGAGAACTTAAAGTTCTTGAAGACCTTGTTCACCCAGGAAGTT	240
Db	181	CTGCTGTAGGAGAGAGAACTTAAAGTTCTTGAAGACCTTGTTCACCCAGGAAGTT	240

Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTCTTTCACCGAGAAATT 240
QY 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCGC 300
Db 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCGC 300
QY 301 TTTCGCCGCCGCCAAAAGACGAGATTTAAACGGGACGTCGGGCCAGAGCTGGGGAA 360
Db 301 TTTCGCCGCCGCCAAAAGACGAGATTTAAACGGGACGTCGGGCCAGAGCTGGGGAA 360
QY 361 ATGGGCCCGAGCCAGGCGCGCTTCTCCTCTGTATGTCCTTTTGCAGACCGCGGTCTTG 420
Db 361 ATGGGCCCGAGCCAGGCGCGCTTCTCCTCTGTATGTCCTTTTGCAGACCGCGGTCTTG 420
QY 421 CAGGGCGCTTGCCTGGTGAGTCCAGGGCTTCGGGGCGAACTAGGGGGCGGGGGGGTG 480
Db 421 CAGGGCGCTTGCCTGGTGAGTCCAGGGCTTCGGGGCGAACTAGGGGGCGGGGGGGTG 480
QY 481 GAAAAATCGAAACTAGCTTTTCTTGGCTTGGGAGTTTGTAACTTTTGGAGGACCTGC 540
Db 481 GAAAAATCGAAACTAGCTTTTCTTGGCTTGGGAGTTTGTAACTTTTGGAGGACCTGC 540
QY 541 TCACCCCTATCCGAAGCCCTCTCCCTACTTCTGTGCTCCAGACCCGCTGAGGAGTGC 600
Db 541 TCACCCCTATCCGAAGCCCTCTCCCTACTTCTGTGCTCCAGACCCGCTGAGGAGTGC 600
QY 601 CTACCACTCAACTGAGATAGGGTCCTCGCCCGAGACCTGCCCTCCCGCGCTGT 660
Db 601 CTACCACTCAACTGAGATAGGGTCCTCGCCCGAGACCTGCCCTCCCGCGCTGT 660
QY 661 CCGGCTCTCGGGAGTGACTTTTGAACCGGCCACTCCCTTCCGCCAACTAGAAATGCTTT 720
Db 661 CCGGCTCTCGGGAGTGACTTTTGAACCGGCCACTCCCTTCCGCCAACTAGAAATGCTTT 720
QY 721 TAAATAAATCTCGTAGTCTTCTCCTCCTGAGCTGAGCTAAGCCTGGGCTCTTGAACCTGG 780
Db 721 TAAATAAATCTCGTAGTCTTCTCCTCCTGAGCTGAGCTAAGCCTGGGCTCTTGAACCTGG 780
QY 781 AACTCGGGTTTATTTCCAAATGACGTGTGAGTGTTCCTCCCACTCATCTCCAAACAGG 840
Db 781 AACTCGGGTTTATTTCCAAATGACGTGTGAGTGTTCCTCCCACTCATCTCCAAACAGG 840
QY 841 AAGTTCTTCCCTGAGTGTGCGGAGAGGCTGAGCAAAACCCAGAGAGATCCGCACGG 900
Db 841 AAGTTCTTCCCTGAGTGTGCGGAGAGGCTGAGCAAAACCCAGAGAGATCCGCACGG 900
QY 901 GGTTCACACTCAGAACGAATCGTTGGGCGGTGGGGCGGAAAGAGTGGCGTTGGGGA 960
Db 901 GGTTCACACTCAGAACGAATCGTTGGGCGGTGGGGCGGAAAGAGTGGCGTTGGGGA 960
QY 961 TCTGAATCTTCCCATTTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCCTAGGT 1020
Db 961 TCTGAATCTTCCCATTTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCCTAGGT 1020
QY 1021 GGGAGCTCCTGAGAGAGGCTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080
Db 1021 GGGAGCTCCTGAGAGAGGCTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080
QY 1081 GCCTGAAAAATTAAATATATAGTTTGTGAACTGTTGAACCTGAACAAATTTCTTTTCGG 1140
Db 1081 GCCTGAAAAATTAAATATATAGTTTGTGAACTGTTGAACCTGAACAAATTTCTTTTCGG 1140
QY 1141 CTAGGCTTATTTGATTTGCAATGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200
Db 1141 CTAGGCTTATTTGATTTGCAATGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200
QY 1201 TAATGAACATGTAAGCAATGCACCTCCTAAGTTACATATCATATCTGATTTATTTGA 1260
Db 1201 TAATGAACATGTAAGCAATGCACCTCCTAAGTTACATATCATATCTGATTTATTTGA 1260
QY 1261 TTTTCACTAGGATAGGGAGGTAGAGCTAAATACGTTTATTTTACTAGAGTTAACT 1320
Db 1261 TTTTCACTAGGATAGGGAGGTAGAGCTAAATACGTTTATTTTACTAGAGTTAACT 1320

QY 1321 GGAATTCAGATTATATAACTCTTTTCAGGTTACAAAGAACATAAATAATCTGTTTTCTG 1380
Db 1321 GGAATTCAGATTATATAACTCTTTTCAGGTTACAAAGAACATAAATAATCTGTTTTCTG 1380
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGGCCTGTAG 1440
Db 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGGCCTGTAG 1440
QY 1441 TGTAGCAGAGTGTCTGTGGGTTCACACCGCGCTTCAGCAGCAGCTTTGAGTTTGGTA 1500
Db 1441 TGTAGCAGAGTGTCTGTGGGTTCACACCGCGCTTCAGCAGCAGCTTTGAGTTTGGTA 1500
QY 1501 CTACGTGTATCCACATTTTACACATGACAAGATGAGGCATGGCAGCCTGCTTCTCGG 1560
Db 1501 CTACGTGTATCCACATTTTACACATGACAAGATGAGGCATGGCAGCCTGCTTCTCGG 1560
QY 1561 CAAATTTATTCAGTACTACCTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
Db 1561 CAAATTTATTCAGTACTACCTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
QY 1621 TATGATTTCTTAAACATCACTGCAATTAGAGGTTGAATAATAAATTTCAATTTGAGCAG 1680
Db 1621 TATGATTTCTTAAACATCACTGCAATTAGAGGTTGAATAATAAATTTCAATTTGAGCAG 1680
QY 1681 AAATATTCATTTTACAAGTSTAATGAGTCCAGGCCATGTGTGCACCTGTTCAAGCCC 1740
Db 1681 AAATATTCATTTTACAAGTSTAATGAGTCCAGGCCATGTGTGCACCTGTTCAAGCCC 1740
QY 1741 CAAGGAGAGAGCAGGGAACAAAGTCTTTACCCTTTTGATATTTTGCATTTCTAGTGGGAG 1800
Db 1741 CAAGGAGAGAGCAGGGAACAAAGTCTTTACCCTTTTGATATTTTGCATTTCTAGTGGGAG 1800
QY 1801 GATGACAATAAGCAATGAGCAGAAAGATATACAACTCAGGAAATCATGGGTCTTCTGA 1860
Db 1801 GATGACAATAAGCAATGAGCAGAAAGATATACAACTCAGGAAATCATGGGTCTTCTGA 1860
QY 1861 GAAGCAGAGAACTCAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGGA 1920
Db 1861 GAAGCAGAGAACTCAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGGA 1920
QY 1921 AATAAGAAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGSCCTGGCAAG 1980
Db 1921 AATAAGAAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGSCCTGGCAAG 1980
QY 1981 TTGGATTTAAAAAGCGGGTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGGG 2040
Db 1981 TTGGATTTAAAAAGCGGGTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGGG 2040
QY 2041 CGCGCTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATCTCTAGCAGTATCCTGT 2100
Db 2041 CGCGCTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATCTCTAGCAGTATCCTGT 2100
QY 2101 CCTCCTACTCACTAGTGCTAGGAGCACTCCCCAGTCTTTGACAACCAAAATGTCTCT 2160
Db 2101 CCTCCTACTCACTAGTGCTAGGAGCACTCCCCAGTCTTTGACAACCAAAATGTCTCT 2160
QY 2161 AAATTTGGCCATGTCACCTAGTAGACAACACTCTCTGTTTAAAGAGCTCGGGTTGAAAA 2220
Db 2161 AAATTTGGCCATGTCACCTAGTAGACAACACTCTCTGTTTAAAGAGCTCGGGTTGAAAA 2220
QY 2221 AATAACAAGTAGTGTGGGAGTAGAGGCCAAGAGTAAATGGCTCAGAAAGAGGA 2280
Db 2221 AATAACAAGTAGTGTGGGAGTAGAGGCCAAGAGTAAATGGCTCAGAAAGAGGA 2280
QY 2281 GCCACAAACAGGTTGTGCGCGCCTGTAGGCTGTGTGTGAATTTCTAGCCAAGGAGTA 2340
Db 2281 GCCACAAACAGGTTGTGCGCGCCTGTAGGCTGTGTGTGAATTTCTAGCCAAGGAGTA 2340
QY 2341 ACAGTCACTGTGCACAGGCTTTTAAAGATTCCTCTGCTGCTATGTGTGAAGAGCAGATG 2400
Db 2341 ACAGTCACTGTGCACAGGCTTTTAAAGATTCCTCTGCTGCTATGTGTGAAGAGCAGATG 2400

Qy	2401	AAGGGAGCAACAGTAAACAGCAGGAGGCCAGCCAGGAAGCTGTATACAGATCCAGGCAAG	2460
Db	2401	AAGGGAGCAACAGTAAACAGCAGGAGGCCAGCCAGGAAGCTGTATACAGATCCAGGCAAG	2460
Qy	2461	AGGTAGTGAGTGGCTGGGTGGCAACAGAAAAGGGAGTGCACAAACCAATGTCTCTCTGAA	2520
Db	2461	AGGTAGTGAGTGGCTGGGTGGCAACAGAAAAGGGAGTGCACAAACCAATGTCTCTCTGAA	2520
Qy	2521	TATATTCTCAAGAAAGTTGCTGTAAGGATTTCTATGTGTGTGAGAGAAAGAGAAGAAATTTGG	2580
Db	2521	TATATTCTCAAGAAAGTTGCTGTAAGGATTTCTATGTGTGTGAGAGAAAGAGAAGAAATTTGG	2580
Qy	2581	CTGGGTGTAGTACTATGCCAAGAGAGAGGCCAAGAGAGCAGATTCCTTGAGCTCAGGA	2640
Db	2581	CTGGGTGTAGTACTATGCCAAGAGAGAGGCCAAGAGAGCAGATTCCTTGAGCTCAGGA	2640
Qy	2641	GTTCAAGACCGCTGGGCAACACAGACAAACCCCTTCTCTACAAAAATACAAAAATTA	2700
Db	2641	GTTCAAGACCGCTGGGCAACACAGACAAACCCCTTCTCTACAAAAATACAAAAATTA	2700
Qy	2701	GCTGGGTGTGGTGGCATGCACCTGTGTATCTACTCGGGAGGCTGAGGTGGAGGTA	2760
Db	2701	GCTGGGTGTGGTGGCATGCACCTGTGTATCTACTCGGGAGGCTGAGGTGGAGGTA	2760
Qy	2761	TTGCTTGACCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTTCAGC	2820
Db	2761	TTGCTTGAGCCCAAGAAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTTCAGC	2820
Qy	2821	CTAGGTGACAGACAGACCCGTCTCCCTTGACCCCTGAAAAGAGAGAGTTAAAGT	2880
Db	2821	CTAGGTGACAGACAGACCCGTCTCCCTTGACCCCTGAAAAGAGAGAGTTAAAGT	2880
Qy	2881	TGACTTTGTCTTTATTTTAAATTTATTGGCTGAGCAGTGGGTAAATGGCAATGCCAT	2940
Db	2881	TGACTTTGTCTTTATTTTAAATTTATTGGCTGAGCAGTGGGTAAATGGCAATGCCAT	2940
Qy	2941	TTCTTGAGATGGTGAAGGCAGAGAAAGACAGTTTGGGGTAAATCAAGGATCTGCATTTG	3000
Db	2941	TTCTTGAGATGGTGAAGGCAGAGAAAGACAGTTTGGGGTAAATCAAGGATCTGCATTTG	3000
Qy	3001	GGACATGTTAAGTTTGAGATTCACAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
Db	3001	GGACATGTTAAGTTTGAGATTCACAGTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
Qy	3061	CAGTGAAGAAATTCAGACCAAGGCTGGGCAGGTGGCTCACTTCTGTAAATCCAGCACT	3120
Db	3061	CAGTGAAGAAATTCAGACCAAGGCTGGGCAGGTGGCTCACTTCTGTAAATCCAGCACT	3120
Qy	3121	TTGGTGGCTGAGGCAGGTAGATCATTTGAGCTCAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
Db	3121	TTGGTGGCTGAGGCAGGTAGATCATTTGAGCTCAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
Qy	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTAGCCCTGGTGGTGCGCGCACGCT	3240
Db	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTAGCCCTGGTGGTGCGCGCACGCT	3240
Qy	3241	ATAGTCCAGGTTTTTCAGGAGGCTTAGGTAGAGAAATCCCTTGAACCCAGGAGGTGCAGG	3300
Db	3241	ATAGTCCAGGTTTTTCAGGAGGCTTAGGTAGAGAAATCCCTTGAACCCAGGAGGTGCAGG	3300
Qy	3301	TTGCAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
Db	3301	TTGCAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
Qy	3361	CTCAAAAAAATAAAAAAAAAAAAAAAAAAATAAGAGAAATTTATCTCAGGATTTGGG	3420
Db	3361	CTCAAAAAAATAAAAAAAAAAAAAAAAAAATAAGAGAAATTTATCTCAGGATTTGGG	3420
Qy	3421	TCTAATTTGCCCTGAGCACCAACTCTCTGAGTTCACTACCATGGCTAGACACACCTTAAAC	3480
Db	3421	TCTAATTTGCCCTGAGCACCAACTCTCTGAGTTCACTACCATGGCTAGACACACCTTAAAC	3480
Qy	3481	ATTTTCTAGAAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATAGATATTGGAATAGAT	3540

Db	3481		ATTTTCTAGAA	CCACACAGCTTTAGTGGAGTCTGCTTAATCATGACTATTGGAATAGGAT	3540
Qy	3541	CTGGGGCAGT	GTAGGGGGTGGCAGCAGTGTGCGAGAGAAAAGCACAAGGAAAGAGC	3600	
Db	3541	CTGGGGCAGT	GTAGGGGGTGGCAGCACCTGTGCGACAGAAAAGCACAAGGAAAGAGC	3600	
Qy	3601	ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTACCCCTTCACAAATGAGGA	3660		
Db	3601	ACCCAGGACTGTCATATGGAAGAAGACAGGACTGCAACTACCCCTTCACAAATGAGGA	3660		
Qy	3661	CCAGACACAGCTGATGGTATGAGTTGATGCAAGGTGTGTGGAGCCTCAACATCCTGCTCC	3720		
Db	3661	CCAGACACAGCTGATGGTATGAGTTGATGCAAGGTGTGTGGAGCCTCAACATCCTGCTCC	3720		
Qy	3721	CTCCTACTACACATGGTTAAGCCCTGTTGCTCTGCTCCAGGTTACACTCTCTCGACATA	3780		
Db	3721	CTCCTACTACACATGGTTAAGCCCTGTTGCTCTGCTCCAGGTTACACTCTCTCGACATA	3780		
Qy	3781	CCTCTCATGGGTGCCCTCAGACAGGACCTTGGCTTCTTCCTTGTGTAAGCTTTGGGCTA	3840		
Db	3781	CCTCTCATGGGTGCCCTCAGACAGGACCTTGGCTTCTTCCTTGTGTAAGCTTTGGGCTA	3840		
Qy	3841	CGTGGATGACACGCTGTCGTGTTCTATGAINATGAGAGTCCGCGTGTGAGCCCCGAAC	3900		
Db	3841	CGTGGATGACACGCTGTCGTGTTCTATGATGATGAGAGTCCGCGTGTGAGCCCCGAAC	3900		
Qy	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGCGCTGCAGCTGAGTCAGAGTCTGAA	3960		
Db	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGCGCTGCAGCTGAGTCAGAGTCTGAA	3960		
Qy	3961	AGGCTGGGATCACATGTTCACTGTTGACTTCTCGACTATTATGAAATCACAAACCACAG	4020		
Db	3961	AGGCTGGGATCACATGTTCACTGTTGACTTCTCGACTATTATGAAATCACAAACCACAG	4020		
Qy	4021	CAAGGATATGGAGAGGGGGCTCACCTTCCTGAGGTTGTGAGCTTTTCATCTTTTC	4080		
Db	4021	CAAGGATATGGAGAGGGGGCTCACCTTCCTGAGGTTGTGAGAGCTTTTCATCTTTTC	4080		
Qy	4081	ATGCATCTGAAGGAAACAGCTGGAAGTCTGAGGTTCTTGTGGGAGCAGGAAGGAAG	4140		
Db	4081	ATGCATCTGAAGGAAACAGCTGGAAGTCTGAGGTTCTTGTGGGAGCAGGAAGGAAG	4140		
Qy	4141	GAATTTGCTTCCCTGAGATCATTTTGGTCTTTGGGATGGTGGAAATAGGGACCTATTTCCTT	4200		
Db	4141	GAATTTGCTTCCCTGAGATCATTTTGGTCTTTGGGATGGTGGAAATAGGGACCTATTTCCTT	4200		
Qy	4201	TGGTTGCAGTTAAACAGGCTGGGGATTTTTCAGAGTCCACACCTCGAGGTCATCTTG	4260		
Db	4201	TGGTTGCAGTTAAACAGGCTGGGGATTTTTCAGAGTCCACACCTCGAGGTCATCTTG	4260		
Qy	4261	GGCTGTGAAATGCAAGAGACAACAGTACCGAGGCTACTTGAAGTACGGGTATGATGGG	4320		
Db	4261	GGCTGTGAAATGCAAGAGACAACAGTACCGAGGCTACTTGAAGTACGGGTATGATGGG	4320		
Qy	4321	CAGGACACACCTTGAAATTTCTGCCCTGACACACTGGATTTGAGAGCAGCAACCCAGGGCC	4380		
Db	4321	CAGGACACACCTTGAAATTTCTGCCCTGACACACTGGATTTGAGAGCAGCAACCCAGGGCC	4380		
Qy	4381	TGGCCCAACAAGCTGGAGTGGGAAAGGACAAGATTCGGGCCAGGCAACAGGGCCCTAC	4440		
Db	4381	TGGCCCAACAAGCTGGAGTGGGAAAGGACAAGATTCGGGCCAGGCAACAGGGCCCTAC	4440		
Qy	4441	CTGGAGAGGACTGCCCTGACACAGCTGCAGAGTTGCTGGAGCTGGGAGAGGTTTGTG	4500		
Db	4441	CTGGAGAGGACTGCCCTGACACAGCTGCAGAGTTGCTGGAGCTGGGAGAGGTTTGTG	4500		
Qy	4501	GACCAACAGGTTAGTGGTGGAAACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560		
Db	4501	GACCAACAGGTTAGTGGTGGAAACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560		
Qy	4561	AGTTTCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTCCTC	4620		
Db	4561	AGTTTCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTCCTC	4620		

Db 4561 AGTTGCGAGGCGACGAATCCCTGGTGTGAGTTTCAGAGGTGGCTGAGGCTGTGTGCTC 4620
QY TCCAAATTTCTGGGAAGGGACTTCTCAATCCCTAGAGTCTCTACCTTATAATTTAGATGTA 4680
Db TCCAAATTTCTGGGAAGGGACTTCTCAATCCCTAGAGTCTCTACCTTATAATTTAGATGTA 4680
QY TGAGACAGCCACAAGTCATGGGTAAATTTCTTTCTCCATGCATATGGCTCAAAAGGAA 4740
Db TGAGACAGCCACAAGTCATGGGTAAATTTCTTTCTCCATGCATATGGCTCAAAAGGAA 4740
QY GTCTCATGGCCCTTCTCTTTTATTAACCAATAATCTTTTGTATATTTATACCTGTAA 4800
Db GTCTCATGGCCCTTCTCTTTTATTAACCAATAATCTTTTGTATATTTATACCTGTAA 4800
QY AAATTCAGAAATGTCAAGCGCGGACCGGTGGCTCACCCCTGTAAATCCCGACACTTTGGG 4860
Db AAATTCAGAAATGTCAAGCGCGGACCGGTGGCTCACCCCTGTAAATCCCGACACTTTGGG 4860
QY AGGCCGAGCGGTGTCTACAAGGTCAGGAGTTTCAGACCCAGCCTGACCAACATGGTGAA 4920
Db AGGCCGAGCGGTGTCTACAAGGTCAGGAGTTTCAGACCCAGCCTGACCAACATGGTGAA 4920
QY ACCCGTCTCTAAAAAATACAAAAATTAGTGGTCACAGTCATGCGCACCTGTAGTCCCA 4980
Db ACCCGTCTCTAAAAAATACAAAAATTAGTGGTCACAGTCATGCGCACCTGTAGTCCCA 4980
QY GCTAATTTGAAGGCTGAGCGAGGCATCGCTTGAACCTGGAGCGAAGTTCACATGA 5040
Db GCTAATTTGAAGGCTGAGCGAGGCATCGCTTGAACCTGGAGCGAAGTTCACATGA 5040
QY GCCAAGATCGCGCACTGCACCTCCAGCCTTAGCGACGAGTGAGACTCCATCTTAAAAA 5100
Db GCCAAGATCGCGCACTGCACCTCCAGCCTTAGCGACGAGTGAGACTCCATCTTAAAAA 5100
QY AAAAAAAGGAGAGATTCAGAGATCTCAGCTATCATATGAATACCAAGACAA 5160
Db AAAAAAAGGAGAGATTCAGAGATCTCAGCTATCATATGAATACCAAGACAA 5160
QY ATATCAAGTGAGGCCACTTATCAGAGTAGAAGAAATCCCTTTAGGTTTAAAAAGTTCTTTCAT 5220
Db ATATCAAGTGAGGCCACTTATCAGAGTAGAAGAAATCCCTTTAGGTTTAAAAAGTTCTTTCAT 5220
QY AGACATAGCAATTAATCACTGAGCTACCTATCTTACAGTCCGCTTCTTATATCAATGTC 5280
Db AGACATAGCAATTAATCACTGAGCTACCTATCTTACAGTCCGCTTCTTATATCAATGTC 5280
QY CTCTAGGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGCACATAA 5340
Db CTCTAGGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGCACATAA 5340
QY AGGCAATTTTATCTATCAGACAAAGACATGGGTACAGATATGTATATTACATGTG 5400
Db AGGCAATTTTATCTATCAGACAAAGACATGGGTACAGATATGTATATTACATGTG 5400
QY AGGAGAACAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTAGAGTCCCAATCTTAGG 5460
Db AGGAGAACAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTAGAGTCCCAATCTTAGG 5460
QY ACACAAATGGTGTCTCTCTGTAGCTGTCTTTTCTGAAAAGGATATTTCTTCCCTCC 5520
Db ACACAAATGGTGTCTCTCTGTAGCTGTCTTTTCTGAAAAGGATATTTCTTCCCTCC 5520
QY AACCTATAGAAGGAAGTGAAGTTCAGTCTTCTGGCAAGGTAACACAGATCCCTCTC 5580
Db AACCTATAGAAGGAAGTGAAGTTCAGTCTTCTGGCAAGGTAACACAGATCCCTCTC 5580
QY CTCACTCTCTCTCTCTCTCAAGTGCCTCTCTTTGGTGAAGGTGACATCATGTGACC 5640
Db CTCACTCTCTCTCTCTCTCAAGTGCCTCTCTTTGGTGAAGGTGACATCATGTGACC 5640
QY TCTTCAGTGACCACTCTACGGTGTGCGGCTTTGAACCTACTACCCCGACCAATCACCATG 5700
Db TCTTCAGTGACCACTCTACGGTGTGCGGCTTTGAACCTACTACCCCGACCAATCACCATG 5700

QY 5701 AAGTGGCTCAAGATGAAGCAGCAATGGATGCCAAGGAGTTTCAACCTAAAGACGTATTG 5760
Db 5701 AAGTGGCTCAAGATGAAGCAGCAATGGATGCCAAGGAGTTTCAACCTAAAGACGTATTG 5760
QY 5761 CCCAATGGGATGGGACCTTACCAGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAG 5820
Db 5761 CCCAATGGGATGGGACCTTACCAGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAG 5820
QY 5821 CAGAGATATACGTTNCCAGGTGGAGCACCAGGCCCTGGATCAGCCCTCATTTGTATCTGG 5880
Db 5821 CAGAGATATACGTTNCCAGGTGGAGCACCAGGCCCTGGATCAGCCCTCATTTGTATCTGG 5880
QY 5881 GGTATGTGACTGATGAGACCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGAGTGCC 5940
Db 5881 GGTATGTGACTGATGAGACCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGAGTGCC 5940
QY 5941 TGAGGAGGTAAATATATGGCAGTGAGATGAGATCTGCTCTTTAGGGGTTGGGCTGAGG 6000
Db 5941 TGAGGAGGTAAATATATGGCAGTGAGATGAGATCTGCTCTTTAGGGGTTGGGCTGAGG 6000
QY 6001 GTGGCAATCAAGGCTTTAACTTGTCTTTTCTGTTTGTAGAGCCCTCACCGTCTGGCAGCC 6060
Db 6001 GTGGCAATCAAGGCTTTAACTTGTCTTTTCTGTTTGTAGAGCCCTCACCGTCTGGCAGCC 6060
QY 6061 TAGTCATTTGAGTCATCAGTGGAAATTTGCTTTTGTGCTCATCTGTTTCATTGGAATTT 6120
Db 6061 TAGTCATTTGAGTCATCAGTGGAAATTTGCTTTTGTGCTCATCTGTTTCATTGGAATTT 6120
QY 6121 TGTTCATAATATTAAGGAAGAGGCGAGGTTTCAAGTGAAGTGAAGCAAGGGGGAAGTCTCT 6180
Db 6121 TGTTCATAATATTAAGGAAGAGGCGAGGTTTCAAGTGAAGTGAAGCAAGGGGGAAGTCTCT 6180
QY 6181 TAGTACTCTGCCCCAGGCACAGTGGGAGAGGCGAGGGGATCTGGCATCCATGGG 6240
Db 6181 TAGTACTCTGCCCCAGGCACAGTGGGAGAGGCGAGGGGATCTGGCATCCATGGG 6240
QY 6241 AAGCATTTTCTCATTTATATTTTCTTTGGGACACCAAGCAGCTCCCTGGGACACAGAAAT 6300
Db 6241 AAGCATTTTCTCATTTATATTTCTTTGGGACACCAAGCAGCTCCCTGGGACACAGAAAT 6300
QY 6301 AATGGTCTTCCCAGATGAAGTCTCTAATTCACAACATCTTCAGAGCACCCTACTAT 6360
Db 6301 AATGGTCTTCCCAGATGAAGTCTCTAATTCACAACATCTTCAGAGCACCCTACTAT 6360
QY 6361 TTTGCAAGAGCTGTTTAAAGTGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
Db 6361 TTTGCAAGAGCTGTTTAAAGTGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
QY 6421 TCTCAGAACCCCAATCTGGTAGGGATGAATTTGATAGCAAGTAAATGTAGTTAAAGAG 6480
Db 6421 TCTCAGAACCCCAATCTGGTAGGGATGAATTTGATAGCAAGTAAATGTAGTTAAAGAG 6480
QY 6481 ACCCCATGAGGTCTTAAAGCAGCAGGAAGCAATGCTTAGGCTGTCAAAGGAAGATG 6540
Db 6481 ACCCCATGAGGTCTTAAAGCAGCAGGAAGCAATGCTTAGGCTGTCAAAGGAAGATG 6540
QY 6541 ATCACAATTCAGCTGGGGATCAAGATAGCCCTCTGGATCTTGAAGGAGAGCTGGATTCCA 6600
Db 6541 ATCACAATTCAGCTGGGGATCAAGATAGCCCTCTGGATCTTGAAGGAGAGCTGGATTCCA 6600
QY 6601 TTAGGTTGAGGTTGAAGATGATGGGAGTCTACACAGCAGGAGCAACCATGCCAAGTAGGA 6660
Db 6601 TTAGGTTGAGGTTGAAGATGATGGGAGTCTACACAGCAGGAGCAACCATGCCAAGTAGGA 6660
QY 6661 GAGTATAAGGCATPACTGGGAGATTAGAAATATTAATCTGTACCTTAACCTGAGTTTGGGT 6720
Db 6661 GAGTATAAGGCATPACTGGGAGATTAGAAATATTAATCTGTACCTTAACCTGAGTTTGGGT 6720
QY 6721 AGCTATCACTCACCAATTTATGCAATTTCTACCCCTGAAACATCTGTGGTGTAGGGAAAAGA 6780
Db 6721 AGCTATCACTCACCAATTTATGCAATTTCTACCCCTGAAACATCTGTGGTGTAGGGAAAAGA 6780

Qy	6781	GAATCAGAAGAAGCCAGCTCATACAGAGTCCAAAGGTCCTTTGGGATATTTGGGTATGA	6840
Db	6781		
		GAATCAGAAGAAGCCAGCTCATACAGAGTCCAAAGGTCCTTTGGGATATTTGGGTATGA	6840
Qy	6841	TCACTGGGTGTCAATTGAAGATCCTAAGAAGGAGCACCACGATCTCCCTTATATGGTG	6900
Db	6841		
		TCACTGGGTGTCAATTGAAGATCCTAAGAAGGAGCACCACGATCTCCCTTATATGGTG	6900
Qy	6901	AATGTGTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTTGAAGGCCAATAAGCAT	6960
Db	6901		
		AATGTGTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCAGTTTGAAGGCCAATAAGCAT	6960
Qy	6961	TTCCAGATGAGAGATAATGGTTCCTTGAATCCATAGTGCACAGGTCTAAATTGAGATGG	7020
Db	6961		
		TTCCAGATGAGAGATAATGGTTCCTTGAATCCATAGTGCACAGGTCTAAATTGAGATGG	7020
Qy	7021	GTGAATGAGGAAAATAAGGAAGAGAGAGCAAGATGGTGCCTAGTTGTTGATGTCCT	7080
Db	7021		
		GTGAATGAGGAAAATAAGGAAGAGAGAGCAAGATGGTGCCTAGTTGTTGATGTCCT	7080
Qy	7081	CTTTCTCGGTCTCTTGTCTCCACAGGAGAGCCATGGGCACTACGCTCTTAGCTGAACG	7140
Db	7081		
		CTTTCTCGGTCTCTTGTCTCCACAGGAGAGCCATGGGCACTACGCTCTTAGCTGAACG	7140
Qy	7141	TGAGTGACGCGACCTGCAGACTCACCTGTGGGAAGGAGACAAACTAGAGACTCAAAGA	7200
Db	7141		
		TGAGTGACGCGACCTGCAGACTCACCTGTGGGAAGGAGACAAACTAGAGACTCAAAGA	7200
Qy	7201	GGGAGTCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTTAAACATAGAAAT	7260
Db	7201		
		GGGAGTCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTTAAACATAGAAAT	7260
Qy	7261	GCCTGAGCACTCCTGATTTTAGCTCTCTGTTCATTTCTCAAAAAGATTTCCCAT	7320
Db	7261		
		GCCTGAGCACTCCTGATTTTAGCTCTCTGTTCATTTCTCAAAAAGATTTCCCAT	7320
Qy	7321	TTAGTTTCTGAGTTCTCGATCCGGTGATCCCTTAGCTGTGACCTCTCCCTGGAACTG	7380
Db	7321		
		TTAGTTTCTGAGTTCTCGATCCGGTGATCCCTTAGCTGTGACCTCTCCCTGGAACTG	7380
Qy	7381	TCTCTCATGAACCTCAAGCTGATCTAGAGGCTTCTTCAATTTCTCCGTCACTCAGAG	7440
Db	7381		
		TCTCTCATGAACCTCAAGCTGATCTAGAGGCTTCTTCAATTTCTCCGTCACTCAGAG	7440
Qy	7441	ACATACACCTATGCTATTTCACTTCTCCTAATTTTGAAGAGGACTCCTTAAATTTGGGGA	7500
Db	7441		
		ACATACACCTATGCTATTTCACTTCTCCTAATTTTGAAGAGGACTCCTTAAATTTGGGGA	7500
Qy	7501	CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCTGGGAGGTGGCTAGTCAT	7560
Db	7501		
		CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCTGGGAGGTGGCTAGTCAT	7560
Qy	7561	AACCTTACCAGATTTTACACATGATCATGCAATTTTCTGGACCCGTTCAACTTTTCT	7620
Db	7561		
		AACCTTACCAGATTTTACACATGATCATGCAATTTTCTGGACCCGTTCAACTTTTCT	7620
Qy	7621	TTGAATCCTCTCTGTGTTTACCAGTAACATCATCTGTGCACCAAGCCTTGGGATTTCT	7680
Db	7621		
		TTGAATCCTCTCTGTGTTTACCAGTAACATCATCTGTGCACCAAGCCTTGGGATTTCT	7680
Qy	7681	CATCTGATTTGATGTCAGTTGCACAGCTATGAAGCTGTACACTGCACGAATGGAAGAG	7740
Db	7681		
		CATCTGATTTGATGTCAGTTGCACAGCTATGAAGCTGTACACTGCACGAATGGAAGAG	7740
Qy	7741	GCACCTGTCCAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTACG	7800
Db	7741		
		GCACCTGTCCAGAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTACG	7800
Qy	7801	AGGTAGGAGCAATATCTTTGAAGGGGTGTGAAGAGGTGTTTTTCTAATTTGGCATGA	7860
Db	7801		
		AGGTAGGAGCAATATCTTTGAAGGGGTGTGAAGAGGTGTTTTTCTAATTTGGCATGA	7860
Qy	7861	AGGTGTCTACAGATTTTGAAGGTTTAATGGTGCCTTCAATTTGGGATGCTCTCTAGTAT	7920

Db	7861	AGGTGCATACAGATTGCAAGTTTAATGGTGCCTTCAATTTGGATGCTACTCTAGTAT	7920
Qy	7921	TCAGACCTTGAAGAATACAATAATTTTCTACCTGGTCTCTCCTTGTCTGATAATAAGAA	7980
Db	7921	TCAGACCTTGAAGAATACAATAATTTTCTACCTGGTCTCTCCTTGTCTGATAATAAGAA	7980
Qy	7981	ATTATGATTAAGATGATATAAAGCACCTTACTTCGTGTCGGACTCTCTTGACGACCTACTTA	8040
Db	7981	ATTATGATTAAGATGATATAAAGCACCTTACTTCGTGTCGGACTCTCTTGACGACCTACTTA	8040
Qy	8041	CATGCATTAATGCATGCACCTCTTACAATAATCTATGAGATAGTACTATTATCCCCAT	8100
Db	8041	CATGCATTAATGCATGCACCTCTTACAATAATCTATGAGATAGTACTATTATCCCCAT	8100
Qy	8101	TTCTTTTAAATGAAGAAAGTGAAGTAGCGCGGCACGGTGGCTCAGCCTGTAAATCCC	8160
Db	8101	TTCTTTTAAATGAAGAAAGTGAAGTAGCGCGGCACGGTGGCTCAGCCTGTAAATCCC	8160
Qy	8161	AGCATTCTGGGAGGCCAAGCGGGTGATCAGAGGTGAGGAGATCAGAGACCACTCCTGGC	8220
Db	8161	AGCATTCTGGGAGGCCAAGCGGGTGATCAGAGGTGAGGAGATCAGAGACCACTCCTGGC	8220
Qy	8221	TAACATGGTGAACCCCATCTCTAATAAAAAATACAAAAATTTAGCTGGGGTGGTGGCAG	8280
Db	8221	TAACATGGTGAACCCCATCTCTAATAAAAAATACAAAAATTTAGCTGGGGTGGTGGCAG	8280
Qy	8281	ACGCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGATGSCATGAACCCAGGAGG	8340
Db	8281	ACGCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGATGSCATGAACCCAGGAGG	8340
Qy	8341	CAGAGCTTGCAGTGAGCCAGTTTGGCCACTGSCACTCCAGCCTAGGTGACAGAGTGAGA	8400
Db	8341	CAGAGCTTGCAGTGAGCCAGTTTGGCCACTGSCACTCCAGCCTAGGTGACAGAGTGAGA	8400
Qy	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATGAAAAAAGAAAGTGAAGTA	8460
Db	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATGAAAAAAGAAAGTGAAGTA	8460
Qy	8461	TAGAGTATCTATAGTTTGTGCAGTGATGAAACAGGTTTCAAACTCAGTCAATCTGACCG	8520
Db	8461	TAGAGTATCTATAGTTTGTGCAGTGATGAAACAGGTTTCAAACTCAGTCAATCTGACCG	8520
Qy	8521	TTTGATACATCTCAGACACCATACATTCAGTAGTTTATAGTGCCTAGATAAATAGAGAA	8580
Db	8521	TTTGATACATCTCAGACACCATACATTCAGTAGTTTATAGTGCCTAGATAAATAGAGAA	8580
Qy	8581	GGAAGAGATGGCTCTCTCTGTCTCATTTGTGTTTCTCTGAGTAGCTTGAATCAAT	8640
Db	8581	GGAAGAGATGGCTCTCTCTGTCTCATTTGTGTTTCTCTGAGTAGCTTGAATCAAT	8640
Qy	8641	GAAGGGAAACAGCAGAAAAACAACCACTGATCCTCAGCTGTCTATGTTTCCCTTTAAAGTC	8700
Db	8641	GAAGGGAAACAGCAGAAAAACAACCACTGATCCTCAGCTGTCTATGTTTCCCTTTAAAGTC	8700
Qy	8701	CCTGAAGGAAGTCTGGAAATGTACTCCCTTGTCTCTGTGCTCTCTTTTGGCATTCA	8760
Db	8701	CCTGAAGGAAGTCTGGAAATGTACTCCCTTGTCTCTGTGCTCTCTTTTGGCATTCA	8760
Qy	8761	TTTCTTTGGACCTTACCAAGGACTGTAAATGGTGGGACAGCTAGTGCCCTCTGCTGGGC	8820
Db	8761	TTTCTTTGGACCTTACCAAGGACTGTAAATGGTGGGACAGCTAGTGCCCTCTGCTGGGC	8820
Qy	8821	TTTACACAGGTGTCTTCCCTAGGCCAGTGCCCTCTGGAATCAGAACTCTGGTGGTATTTC	8880
Db	8821	TTTACACAGGTGTCTTCCCTAGGCCAGTGCCCTCTGGAATCAGAACTCTGGTGGTATTTC	8880
Qy	8881	CCTCAATGAAGTGAGTAAGCTCTCTCATTTTTCAGATGTTAATGAAGCCCAAGTG	8940
Db	8881	CCTCAATGAAGTGAGTAAGCTCTCTCATTTTTCAGATGTTAATGAAGCCCAAGTG	8940
Qy	8941	GCTTAGAGGATGCCAGGTCTTCCATGTGAGGCACCTGGGGTTCGGGTGCACATTAATAA	9000

BASE COUNT		2999 a	2252 c	2648 g	2926 t				
ORIGIN									
Query Match		100.0%;		Score 10823;		DB 6;		Length 10825;	
Best Local Similarity		100.0%;		Pred. No. 0;					
Matches 10823;		Conservative		0; Mismatches		2; Indels		0; Gaps	
		0;							
Qy	1	TCTAAGTTGAGATAAATTTTAAATGTATGATGAATTTTGAATAATCATATAATATTTA	60						
Db	1	TCTAAGTTGAGATAAATTTTAAATGTATGATGAATTTTGAATAATCATATAATATTTA	60						
Qy	61	AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAACACCCCT	120						
Db	61	AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAACACCCCT	120						
Qy	121	TCAGAGTTTAAACCAAGAGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT	180						
Db	121	TCAGAGTTTAAACCAAGAGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT	180						
Qy	181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACTGTGCTTTTCACCAAGGAAGTT	240						
Db	181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACTGTGCTTTTCACCAAGGAAGTT	240						
Qy	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG	300						
Db	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG	300						
Qy	301	TTTCCCGCCCCCAAAAGAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAA	360						
Db	301	TTTCCCGCCCCCAAAAGAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAA	360						
Qy	361	ATGGGCGCGGAGCGCGGCTTCTCCTCTGATGCTATTTTCAGACCGCGGTCCTG	420						
Db	361	ATGGGCGCGGAGCGCGGCTTCTCCTCTGATGCTATTTTCAGACCGCGGTCCTG	420						
Qy	421	CAGGGGCGGTTGCTGCGTAGTTCAGGGCTGCGGGCGAATAGGGGCGCGGGGGTG	480						
Db	421	CAGGGGCGGTTGCTGCGTAGTTCAGGGCTGCGGGCGAATAGGGGCGCGGGGGTG	480						
Qy	481	GAATAATCGAACTAGCTTTTCTTGGCTTGGAGTTGCTAACTTTGAGGACCTGC	540						
Db	481	GAATAATCGAACTAGCTTTTCTTGGCTTGGAGTTGCTAACTTTGAGGACCTGC	540						
Qy	541	TCAACCCCTATCCGCAAGCCCTCTCCCTACTTTCTGCTTCCAGACCCCGTGAGGAGTGC	600						
Db	541	TCAACCCCTATCCGCAAGCCCTCTCCCTACTTTCTGCTTCCAGACCCCGTGAGGAGTGC	600						
Qy	601	CTACCACTGAATGCAGATAGGGTCCCTCGCCCGCAGGACCTGCCCTCCCGGCTGT	660						
Db	601	CTACCACTGAATGCAGATAGGGTCCCTCGCCCGCAGGACCTGCCCTCCCGGCTGT	660						
Qy	661	CCGGCTCTGCGGAGTGTACTTTTGAACCGCCCACTCCCTTCCGCCAACTAGAATGCTTT	720						
Db	661	CCGGCTCTGCGGAGTGTACTTTTGAACCGCCCACTCCCTTCCGCCAACTAGAATGCTTT	720						
Qy	721	TAAATAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCCTGGGGCTCCTTGAACCTGG	780						
Db	721	TAAATAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCCTGGGGCTCCTTGAACCTGG	780						
Qy	781	AACCTCGGTTTATTTCCCAATGTACGTGTGCAGTTTTCCTCCAGTCACTCCAAACAGG	840						
Db	781	AACCTCGGTTTATTTCCCAATGTACGTGTGCAGTTTTCCTCCAGTCACTCCAAACAGG	840						
Qy	841	AAGTTCTTCCCTGAGTGTGTCGAGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	900						
Db	841	AAGTTCTTCCCTGAGTGTGTCGAGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	900						
Qy	901	GGTTTCCACCTCAGAACGAATCGTTTGGCGGTGGGGCGCGAAGAGTGGGTTGGGA	960						
Db	901	GGTTTCCACCTCAGAACGAATCGTTTGGCGGTGGGGCGCGAAGAGTGGGTTGGGA	960						
Qy	961	TCTGAATTTCTTACCATTCCACCCACTTTTGGTGTAGACCTTGGGGTGGAGGTCCTTAGGGT	1020						

Db	961																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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Db 2041 CGCGGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTTAGCAGTATCCTGT 2100
QY 2101 CTTCCCTACTACTAGGTGCTAGGAGCACTCCCCAGTCTTGACACCAAAAATGTCTCT 2160
Db 2101 CTTCCCTACTACTAGGTGCTAGGAGCACTCCCCAGTCTTGACACCAAAAATGTCTCT 2160
QY 2161 AAATTTGGCACATGTCACCTAGTAGACAAACACTCTCTGTTAAAGAGTCGGGTTGAAAA 2220
Db 2161 AAATTTGGCACATGTCACCTAGTAGACAAACACTCTCTGTTAAAGAGTCGGGTTGAAAA 2220
QY 2221 AATAACAAGTAGTGTGGGAGTAGAGGCCAAGAAGTAGTAAATGGGCTCAGAAAGGA 2280
Db 2221 AATAACAAGTAGTGTGGGAGTAGAGGCCAAGAAGTAGTAAATGGGCTCAGAAAGGA 2280
QY 2281 GCCACAAACAAGTTGTGCAGCGCCTGTAGGCTGTGTGTGAATTTAGCCAAAGGAGTA 2340
Db 2281 GCCACAAACAAGTTGTGCAGCGCCTGTAGGCTGTGTGTGAATTTAGCCAAAGGAGTA 2340
QY 2341 ACAGTCATCTGTACAGGCTTTAAAGATTGCTCTGGCTGCTATGTGGAAACAGAAATG 2400
Db 2341 ACAGTCATCTGTACAGGCTTTAAAGATTGCTCTGGCTGCTATGTGGAAACAGAAATG 2400
QY 2401 AAGGGAGCAACAGTAAAGAGCGGAGCCAGCCAGGAAGCTTTACACAGTCCAGGCAAG 2460
Db 2401 AAGGGAGCAACAGTAAAGAGCGGAGCCAGCCAGGAAGCTTTACACAGTCCAGGCAAG 2460
QY 2461 AGGTAGTGAGTGGCTGGGTGGGACAGAAAGGGAGTGACAAACCATTTGCTCTCGAA 2520
Db 2461 AGGTAGTGAGTGGCTGGGTGGGACAGAAAGGGAGTGACAAACCATTTGCTCTCGAA 2520
QY 2521 TATATTCTGAAGGAATTTGCTGAAGGATTTCTATGTTGTGAGAGAAAGAGAAATGG 2580
Db 2521 TATATTCTGAAGGAATTTGCTGAAGGATTTCTATGTTGTGAGAGAAAGAGAAATGG 2580
QY 2581 CTGGGTGAGTGCATGCCAAGAGAGAGCGCCAGAGGACAGATTCCTGAGCTCAGGA 2640
Db 2581 CTGGGTGAGTGCATGCCAAGAGAGAGCGCCAGAGGACAGATTCCTGAGCTCAGGA 2640
QY 2641 GTTCAAGACAGCCTGGGCAACACAGCAAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
Db 2641 GTTCAAGACAGCCTGGGCAACACAGCAAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
QY 2701 GCTGGGTGGTGGATGCACCTGTATCTAGTACTCGGAGGCTGAGGTGAGGGTA 2760
Db 2701 GCTGGGTGGTGGATGCACCTGTATCTAGTACTCGGAGGCTGAGGTGAGGGTA 2760
QY 2761 TTGCTTGAGCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC 2820
Db 2761 TTGCTTGAGCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC 2820
QY 2821 CTAGGTGACAGAGAGACCCCTGCTCCCTGACCCCTGAAAAGACAGAGTTAAAGT 2880
Db 2821 CTAGGTGACAGAGAGACCCCTGCTCCCTGACCCCTGAAAAGACAGAGTTAAAGT 2880
QY 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAATGGCAATGCCAT 2940
Db 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAATGGCAATGCCAT 2940
QY 2941 TTCTGAGATGGTCAAGGACAGAGAGAGTGGGTGAAATCAAGGATCTGCATTTG 3000
Db 2941 TTCTGAGATGGTCAAGGACAGAGAGAGTGGGTGAAATCAAGGATCTGCATTTG 3000
QY 3001 GGCATGTTAAAGTTTGAGATTTCCAGTCAAGGCTTCCAAAGTGTGAGGCCACATAGGCAGTT 3060
Db 3001 GGCATGTTAAAGTTTGAGATTTCCAGTCAAGGCTTCCAAAGTGTGAGGCCACATAGGCAGTT 3060
QY 3061 CAGTGTAAAGATTCAGGACCAAGGCTGGCAGGCTGCTCTCTCTAATCCAGACT 3120
Db 3061 CAGTGTAAAGATTCAGGACCAAGGCTGGCAGGCTGCTCTCTCTAATCCAGACT 3120
QY 3121 TTGGTGGCTGAGGACAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGCGCAACA 3180
Db 3121 TTGGTGGCTGAGGACAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCTTGCGCAACA 3180

QY 3181 TGGTGAACCCCAITGCTACTAAAAATACAAAAATAGCCTGGTGTGGTGGCGCACGCCT 3240
Db 3181 TGGTGAACCCCAITGCTACTAAAAATACAAAAATAGCCTGGTGTGGTGGCGCACGCCT 3240
QY 3241 ATAGTCCCAGTGTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAACCCAGGAGTGCAGG 3300
Db 3241 ATAGTCCCAGTGTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAACCCAGGAGTGCAGG 3300
QY 3301 TTGCAGTGAAGTGAAGATTTGCCACTGCCACTCCAGCCTGGGTGATAGAGTGAAGTCTGT 3360
Db 3301 TTGCAGTGAAGTGAAGATTTGCCACTGCCACTCCAGCCTGGGTGATAGAGTGAAGTCTGT 3360
QY 3361 CTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3420
Db 3361 CTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3420
QY 3421 TCTAATTTGCCCTGACACCAACTCTGAGTCAACTACCATGGCTAGACACACCTTAAC 3480
Db 3421 TCTAATTTGCCCTGACACCAACTCTGAGTTCAACTACCATGGCTAGACACACCTTAAC 3480
QY 3481 ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 3540
Db 3481 ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 3540
QY 3541 CTGGGGCAGTGAAGGGTGGCAGCCAGCTGTGGCAGAGAAAGACACACAGGAAGAGC 3600
Db 3541 CTGGGGCAGTGAAGGGTGGCAGCCAGCTGTGGCAGAGAAAGACACACAGGAAGAGC 3600
QY 3601 ACCAGGACTGTCTATATGGAAGAAAGACAGGACTCAACTCACCTTTCACAAAATGAGGA 3660
Db 3601 ACCAGGACTGTCTATATGGAAGAAAGACAGGACTCAACTCACCTTTCACAAAATGAGGA 3660
QY 3661 CCAGACACAGCTCATGATGAGTTGATGAGTGTGGAGCTTCAACATCTCTGCTCCC 3720
Db 3661 CCAGACACAGCTCATGATGAGTTGATGAGTGTGGAGCTTCAACATCTCTGCTCCC 3720
QY 3721 CTCTACTACACATGTTTAAAGCCTTGTCTCTCTCCAGGTTTCACACTCTCTGCACTA 3780
Db 3721 CTCTACTACACATGTTTAAAGCCTTGTCTCTCTCCAGGTTTCACACTCTCTGCACTA 3780
QY 3781 CCTCTCATGGGCTCAGACGAGCACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840
Db 3781 CCTCTCATGGGCTCAGACGAGCACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840
QY 3841 CGTGGATGACCAAGTCT 3900
Db 3841 CGTGGATGACCAAGTCT 3900
QY 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTCAGCTGAGCTGAGTCTGAA 3960
Db 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTCAGCTGAGCTGAGTCTGAA 3960
QY 3961 AGGTGGGATCAGATGTTTCACTGTTGACTTCTGGACTATTATGAAAAATCAACACCAG 4020
Db 3961 AGGTGGGATCAGATGTTTCACTGTTGACTTCTGGACTATTATGAAAAATCAACACCAG 4020
QY 4021 CAAGGTATGTGAGAGGGGCTCACCCTCTGAGTGTGTCAGAGCTTTTCATCTTTTC 4080
Db 4021 CAAGGTATGTGAGAGGGGCTCACCCTCTGAGTGTGTCAGAGCTTTTCATCTTTTC 4080
QY 4081 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 4140
Db 4081 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 4140
QY 4141 GAATTTGCTTCTCCAGATCATTTGGTCCCTGGGATGCTGGAAATAGGACCTATTCTTT 4200
Db 4141 GAATTTGCTTCTCCAGATCATTTGGTCCCTGGGATGCTGGAAATAGGACCTATTCTTT 4200
QY 4201 TGGTTCAGTTAAAGGCTGGGATTTTCCAGAGTCCCAACCCCTGCAGGTCATCTG 4260
Db 4201 TGGTTCAGTTAAAGGCTGGGATTTTCCAGAGTCCCAACCCCTGCAGGTCATCTG 4260

Db 6421 TCTCAGAACCCAAATCTGGTAGGAATGAAATTGATAGCAAGTAAATCTAGTTAAAGAAG 6480
QY 6481 ACCCATGAGGTCTTAAAGCAGCGAGGAAGCAAAATGCTTAGGGTCTCAAGCAAGAATG 6540
Db 6481 ACCCATGAGGTCTTAAAGCAGCGAGGAAGCAAAATGCTTAGGGTCTCAAGCAAGAATG 6540
QY 6541 ATCACATTCAGCTGGGGATCAAGATAGCCTCTGATCTTTGAAGGAGAGCTTGGATTCCA 6600
Db 6541 ATCACATTCAGCTGGGGATCAAGATAGCCTCTGATCTTTGAAGGAGAGCTTGGATTCCA 6600
QY 6601 TTAGGTGAGGTTGAAGATGATGGGAGGTCACACAGACGGAGCAACATGCCAAGTAGGA 6660
Db 6601 TTAGGTGAGGTTGAAGATGATGGGAGGTCACACAGACGGAGCAACATGCCAAGTAGGA 6660
QY 6661 GAGTATAAGGCATCTCTGGGAGATTAGAATAATTACTGTACTTAAACCTCAGTTTGGGT 6720
Db 6661 GAGTATAAGGCATCTCTGGGAGATTAGAATAATTACTGTACTTAAACCTCAGTTTGGGT 6720
QY 6721 AGCTATCACTACCAATATATGCAATTTACCCCTTGAACATCTGTGGTGTAGGGAAGA 6780
Db 6721 AGCTATCACTACCAATATATGCAATTTACCCCTTGAACATCTGTGGTGTAGGGAAGA 6780
QY 6781 GAATCAGAAAGACCGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTATGA 6840
Db 6781 GAATCAGAAAGACCGCTCATACAGAGTCCAAGGGTCTTTTGGGATATTGGGTATGA 6840
QY 6841 TCACCTGGGGTGTCAATTGAAGATCTTAAGAAAGGAGGACCAGATCTCCCTTATATGGTG 6900
Db 6841 TCACCTGGGGTGTCAATTGAAGATCTTAAGAAAGGAGGACCAGATCTCCCTTATATGGTG 6900
QY 6901 AATGTGTTTGAAGTTAGATGAGAGGTGAGGAGCCAGTTTGAAGCCCAATTAAGCAT 6960
Db 6901 AATGTGTTTGAAGTTAGATGAGAGGTGAGGAGCCAGTTTGAAGCCCAATTAAGCAT 6960
QY 6961 TTCCAGATGAGAGATAATGGTTCTTGAATCCAATAGTGCACAGTCTAATTTAGATGG 7020
Db 6961 TTCCAGATGAGAGATAATGGTTCTTGAATCCAATAGTGCACAGTCTAATTTAGATGG 7020
QY 7021 GTGAATGAGGAAATTAAGGAAGAGAGAGCAAGATGTTGCCCTTAGTATGCCCT 7080
Db 7021 GTGAATGAGGAAATTAAGGAAGAGAGAGCAAGATGTTGCCCTTAGTATGCCCT 7080
QY 7081 CTTTCCCTGGGTCTCTGTCTCCACAGGAGGAGCCATGGGGCAGCTTAGCTGTGAAGC 7140
Db 7081 CTTTCCCTGGGTCTCTGTCTCCACAGGAGGAGCCATGGGGCAGCTTAGCTGTGAAGC 7140
QY 7141 TGAGTGACACGACGCTCGACACTCAGTGTGGGAAGGAGACAAACTAGAGACTCAAAGA 7200
Db 7141 TGAGTGACACGACGCTCGACACTCAGTGTGGGAAGGAGACAAACTAGAGACTCAAAGA 7200
QY 7201 GGGAGTGCAATTTATGAGCTCTTCATGTTTCAGGAGAGATTGAACCTTAAACATAGAAAT 7260
Db 7201 GGGAGTGCAATTTATGAGCTCTTCATGTTTCAGGAGAGATTGAACCTTAAACATAGAAAT 7260
QY 7261 GCCTGACCAACTCCTTTGATTTTAGCTCTCTGTCTCATTTTCTCAAAAAGATTTCCCCAT 7320
Db 7261 GCCTGACCAACTCCTTTGATTTTAGCTCTCTGTCTCATTTTCTCAAAAAGATTTCCCCAT 7320
QY 7321 TTAGGTTTCTGAGTTCCTGATGCGGTGATCCCTAGCTGTGACCTCTCCCTGGAACCTG 7380
Db 7321 TTAGGTTTCTGAGTTCCTGATGCGGTGATCCCTAGCTGTGACCTCTCCCTGGAACCTG 7380
QY 7381 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCAATTCCTCCGTCACCTCAGAG 7440
Db 7381 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCAATTCCTCCGTCACCTCAGAG 7440
QY 7441 ACATACACCTATGTCATTTTCAATTTTCCCTATTTTGAAGAGGACTCCCTTAAATTTGGGGGA 7500
Db 7441 ACATACACCTATGTCATTTTCAATTTTCCCTATTTTGAAGAGGACTCCCTTAAATTTGGGGGA 7500
QY 7501 CTTACATGATTTCAATTTTAAACATCTGAGAAAAGCTTTTGAACCTGGGAGCTGGCTAGTCAT 7560
Db 7501 CTTACATGATTTCAATTTTAAACATCTGAGAAAAGCTTTTGAACCTGGGAGCTGGCTAGTCAT 7560

QY 7561 AACCTTACCAGATTTTTTACACATGTATCTATGCAATTTTCTGGACCCGTTCAACTTTTCCT 7620
Db 7561 AACCTTACCAGATTTTTTACACATGTATCTATGCAATTTTCTGGACCCGTTCAACTTTTCCT 7620
QY 7621 TTGAATCCTCTCTCTGTGTTTACCAGTAACCTCATCTGTACCAAGCCTTGGGATCTTTC 7680
Db 7621 TTGAATCCTCTCTCTGTGTTTACCAGTAACCTCATCTGTACCAAGCCTTGGGATCTTTC 7680
QY 7681 CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740
Db 7681 CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740
QY 7741 GCACCTCTCCAGAAAAGCATCATGCCATCTCTGGGTAGTATGATGGGTGTTTATAGC 7800
Db 7741 GCACCTCTCCAGAAAAGCATCATGCCATCTCTGGGTAGTATGATGGGTGTTTATAGC 7800
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Db 7801 AGGTAGGAGCAATATCTTTGAAAGGGTGTGAAGAGGTGTTTTTCTAATTTGGCATGA 7860
QY 7861 AGGTGTCATACAGATTTGCAAGGTTTAAGGTGCCCTTCATTTGGGATGCTTCTAGTAT 7920
Db 7861 AGGTGTCATACAGATTTGCAAGGTTTAAGGTGCCCTTCATTTGGGATGCTTCTAGTAT 7920
QY 7921 TCCAGACCTCAAGAAATCACAATAATTTTCTACCTGGTCTCTCCTTCTGTGATAATCAAA 7980
Db 7921 TCCAGACCTCAAGAAATCACAATAATTTTCTACCTGGTCTCTCCTTCTGTGATAATCAAA 7980
QY 7981 ATTATGATAAGGATGATAAAGCACTTACTTTCGTGCCGACTCTTCTGAGCACTACTTA 8040
Db 7981 ATTATGATAAGGATGATAAAGCACTTACTTTCGTGCCGACTCTTCTGAGCACTACTTA 8040
QY 8041 CATGCAATTACTGATGCACCTTCTTACAATAATTTCTATGAGATAGGTACTATTATCCCAT 8100
Db 8041 CATGCAATTACTGATGCACCTTCTTACAATAATTTCTATGAGATAGGTACTATTATCCCAT 8100
QY 8101 TTTCTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACCCCTGTAATCCC 8160
Db 8101 TTTCTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACCCCTGTAATCCC 8160
QY 8161 AGCACTTTGGGAGGCCAAAGCGGTGGATACAGAGTCAAGGATCCGAGACCATCCTGCG 8220
Db 8161 AGCACTTTGGGAGGCCAAAGCGGTGGATACAGAGTCAAGGATCCGAGACCATCCTGCG 8220
QY 8221 TAACATGGTGAACCCCATCTCTTAATAAATAACAAAATTAGCTGGCGGTGGTGGCAG 8280
Db 8221 TAACATGGTGAACCCCATCTCTTAATAAATAACAAAATTAGCTGGCGGTGGTGGCAG 8280
QY 8281 ACCCTGTAGTCCCAGCTACTCGGAAGGCTGAGCGCAGGAGATGGCATGAACCCAGGAGG 8340
Db 8281 ACCCTGTAGTCCCAGCTACTCGGAAGGCTGAGCGCAGGAGATGGCATGAACCCAGGAGG 8340
QY 8341 CAGAGCTTGCAGTGACCGAGTTTGGCCAGCTGCACCTCCAGCCTAGGTGACAGAGTGAGA 8400
Db 8341 CAGAGCTTGCAGTGACCGAGTTTGGCCAGCTGCACCTCCAGCCTAGGTGACAGAGTGAGA 8400
QY 8401 CTCACCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 8460
Db 8401 CTCACCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 8460
QY 8461 TAGAGTATCTCATPAGTTTGTCTAGTGTAGAGAACAGGTTTCAAACCTCAGTCAATCTGACCG 8520
Db 8461 TAGAGTATCTCATPAGTTTGTCTAGTGTAGAGAACAGGTTTCAAACCTCAGTCAATCTGACCG 8520
QY 8521 TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCCTAGATAAATAGAGAA 8580
Db 8521 TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCCTAGATAAATAGAGAA 8580
QY 8581 GGAAGGAGATGGCTCTTCTTCTGTCTCATTTGTTTCTCTGAGTCAGCTTCAATCAGAT 8640
Db 8581 GGAAGGAGATGGCTCTTCTTCTGTCTCATTTGTTTCTTCTCTGAGTCAGCTTGAATCAGAT 8640

Qy	8641	GAAGGGGAACACGAGAAACAAACCAACTGATCCTCAGCTGTCATGTTCTCTTTAAAGTC	8700
Db	8641	GAAGGGGAACACGAGAAACAAACCAACTGATCCTCAGCTGTCATGTTCTCTTTAAAGTC	8700
	8701	CCTGAAGGAAGTCTCGGAATGTGACTCCCTTGCTCTCTGTTGCTCTCTTTGGCAATCA	8760
Db	8701	CCTGAAGGAAGTCTCGGAATGTGACTCCCTTGCTCTCTGTTGCTCTCTTTGGCAATCA	8760
	8761	TTTCTTTGGACCTACGCAAGGACTGTAAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGG	8820
Db	8761	TTTCTTTGGACCTACGCAAGGACTGTAAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGG	8820
	8821	TTTCACACGSGTCTCCTCCCTAGGCCAGTGCTCTGAGTCAAGAACTCTGCTGCTGCTATTTT	8880
Db	8821	TTTCACACGSGTCTCCTCCCTAGGCCAGTGCTCTGAGTCAAGAACTCTGCTGCTGCTATTTT	8880
	8881	CCTCAATGAAGTGGAGTAAAGTCTCTCAATTTTGAGATGGTATATGAAAGCCACCAAGTG	8940
Db	8881	CCTCAATGAAGTGGAGTAAAGTCTCTCAATTTTGAGATGGTATATGAAAGCCACCAAGTG	8940
	8941	GCTTAGAGATGCCAGGTCCTTCCATGGAGCCACTGGGGTTCGGTGCACATTAATAAAA	9000
Db	8941	GCTTAGAGATGCCAGGTCCTTCCATGGAGCCACTGGGGTTCGGTGCACATTAATAAAA	9000
	9001	AAAACTCTAACAGGACATTCAGGAATTCGTAGATTTCTGGGAAATCAGTTCACCATGTTCA	9060
Db	9001	AAAACTCTAACAGGACATTCAGGAATTCGTAGATTTCTGGGAAATCAGTTCACCATGTTCA	9060
	9061	AAAGAGTCTTTTTTTTTTTTTTTTGAGACTCTATATGCCAGGCTGGAGTGCAAATGGCATGAT	9120
Db	9061	AAAGAGTCTTTTTTTTTTTTTTTTGAGACTCTATATGCCAGGCTGGAGTGCAAATGGCATGAT	9120
	9121	CTCGGCTCACTGTAACTCTGCCTCCAGGTTCAAGCGATTCTCCTCTCTCAGCTCCCA	9180
Db	9121	CTCGGCTCACTGTAACTCTGCCTCCAGGTTCAAGCGATTCTCCTCTCTCAGCTCCCA	9180
	9181	AGTAGCTGGGATTACAGGCGTGCACCCACCATGCCCGGCTAAATTTTGTATTTTAGTAGA	9240
Db	9181	AGTAGCTGGGATTACAGGCGTGCACCCACCATGCCCGGCTAAATTTTGTATTTTAGTAGA	9240
	9241	GACAGSGTTTCACCATGTTGGCAGSGTGGTCTCGAACTCTCCTGACTCGTGATCGCC	9300
Db	9241	GACAGSGTTTCACCATGTTGGCAGSGTGGTCTCGAACTCTCCTGACTCGTGATCGCC	9300
	9301	TGCCTCGGCCCTCCAAAGTGCTGAGATTACAGGTGTAGCCACCCTGCCAGCGCTCAAA	9360
Db	9301	TGCCTCGGCCCTCCAAAGTGCTGAGATTACAGGTGTAGCCACCCTGCCAGCGCTCAAA	9360
	9361	AGAGTCTTAATATATATATCCAGATGGCATGTGTTACTTTTATGTTACTACATGCACATT	9420
Db	9361	AGAGTCTTAATATATATCCAGATGGCATGTGTTACTTTATGTTACTACATGCACATT	9420
	9421	GCTGSCATAAATGGTACAAGCATTTCTGTCTGAAGGCGAGGTGCTTCAGGATACCATAT	9480
Db	9421	GCTGSCATAAATGGTACAAGCATTTCTGTCTGAAGGCGAGGTGCTTCAGGATACCATAT	9480
	9481	ACAGCTCAGAAGTTTCTCTTTTAGGCATTAAATTTTAGCAAGATATCTCATCTCTCTT	9540
Db	9481	ACAGCTCAGAAGTTTCTCTTTTAGGCATTAAATTTTAGCAAGATATCTCATCTCTCTT	9540
	9541	TTAAACCATTTCTTTTTTTTGGTGTAGAAAAGTTATGTAAGAAAAAGTAAATCTGATTT	9600
Db	9541	TTAAACCATTTCTTTTTTTTGGTGTAGAAAAGTTATGTAAGAAAAAGTAAATCTGATTT	9600
	9601	ACGCTCATTTAGAAAAGCTATAAAAATGAATACAAATTAAGCTGTTATTTAATTAGCCAG	9660
Db	9601	ACGCTCATTTAGAAAAGCTATAAAAATGAATACAAATTAAGCTGTTATTTAATTAGCCAG	9660
	9661	TGAAAAACTATTAAACAACTGTCTATTACCTGTTAGTATTATTGTTGCATTAATAAATGCA	9720
Db	9661	TGAAAAACTATTAAACAACTGTCTATTACCTGTTAGTATTATTGTTGCATTAATAAATGCA	9720
	9721	TATACTTTTAATAAATGTATATTGTATGTATACTGCATGATTTTATTAAGCTCTCTGTC	9780

Db	9721	TATACCTTTAAATAAAGFRAATATGTAATGTATPACATGCAATATTTATTATTGAAGTCTCTGTTCT	9780
Qy	9781	ATCTTGTGTATATACCTTAATCGCTTGTGTCATTTTGGAGACATTTATTTTGCTCTCAATTT	9840
Db	9781	ATCTTGTGTATATACCTTAATCGCTTGTGTCATTTTGGAGACATTTATTATTGCTCTCAATTT	9840
Qy	9841	CTTTACATTTTGTCTTACGGGAATATTTTCATTTCAACTGCTGAGCCGAATTAATTCSTGTT	9900
Db	9841	CTTTACATTTTGTCTTACGGGAATATTTTCATTTCAACTGCTGAGCCGAATTAATTCSTGTT	9900
Qy	9901	TCTTCACCTCTAGGACATTTGCTGCTAAGTTGTGAAGACATTTGGTTATTTTACCAGCAAC	9960
Db	9901	TCTTCACCTCTAGGACATTTGCTGCTAAGTTGTGAAGACATTTGGTTATTTTACCAGCAAC	9960
Qy	9961	CATTCCTGAAGCATATGACAAATTAATTTCTCTCTTAATACTTTACTATCTGAAAGCAGA	10020
Db	9961	CATTCCTGAAGCATATGACAAATTAATTTCTCTCTTAATACTTTACTATCTGAAAGCAGA	10020
Qy	10021	CTGCTATTAAGGCTTCACATTCTCTACCTCATTAAGGAATGTGTACAAATTAATTTATT	10080
Db	10021	CTGCTATTAAGGCTTCACATTCTCTACCTCATTAAGGAATGTGTACAAATTAATTTATT	10080
Qy	10081	AGGTGAAGCATTTGTTTTATATATGGTTTTATTCTACCTGGGTGAGATTTCAAGAAACACC	10140
Db	10081	AGGTGAAGCATTTGTTTTATATATGGTTTTATTCTACCTGGGTGAGATTTCAAGAAACACC	10140
Qy	10141	CCAGTCTTCACAGTAACACATTTCTACTAACACATTTACTTAACATTCAGCAACTGTGGCT	10200
Db	10141	CCAGTCTTCACAGTAACACATTTCTACTAACACATTTACTTAACATTCAGCAACTGTGGCT	10200
Qy	10201	GTTAAATTTTTTAAATAGAAATTTTAAGTCCTCATTTCTCTCGGTGTTTTTAAAGCTTAA	10260
Db	10201	GTTAAATTTTTTAAATAGAAATTTTAAGTCCTCATTTCTCTCGGTGTTTTTAAAGCTTAA	10260
Qy	10261	TTTTTCTGGCTTTATTCATAAATCTTAAGGTCAACTACATTTGAAAATCAAGACCTG	10320
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Qy	10321	CATTTTAAATCTTATTCACCTCTGGCAAAACCATTCACAAACCATGTTAGTAAGAGAA	10380
Db	10321	CATTTTAAATCTTATTCACCTCTGGCAAAACCATTCACAAACCATGTTAGTAAGAGAA	10380
Qy	10381	GGGTGACACCTGGTGGCCATAGGTAATGTACCACGGTGGTCCGGTGACCAAGATGCAG	10440
Db	10381	GGGTGACACCTGGTGGCCATAGGTAATGTACCACGGTGGTCCGGTGACCAAGATGCAG	10440
Qy	10441	CGCTGAGGGTTTTCTGAAAGTAAAGGAATAAGAAATGGGTGGAGGGCGCTGCATCGAA	10500
Db	10441	CGCTGAGGGTTTTCTGAAAGTAAAGGAATAAGAAATGGGTGGAGGGCGCTGCATCGAA	10500
Qy	10501	ATCAGTTGTAGAGAAAGCCCTGAAAATTTTGAGAAAACAAACAGAACTACTTTACCAG	10560
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Qy	10561	CTATTGTAAATTCCTGGAATCAGGCCATTTGCTGAGCTGCCCTGAACTGGGAACACAAACAG	10620
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Qy	10621	AAGGAAAACAAACCACTCTGTAATCATTTGAGTCAAGTACAGCAGGTGATTGAGGACTGC	10680
Db	10621	AAGGAAAACAAACCACTCTGTAATCATTTGAGTCAAGTACAGCAGGTGATTGAGGACTGC	10680
Qy	10681	TGAGAGGTACAGCCAAAATTTCTTATGTTGTTATTATAATATGTCATCTTATAATACTGT	10740
Db	10681	TGAGAGGTACAGCCAAAATTTCTTATGTTGTTATTATAATATGTCATCTTATAATACTGT	10740
Qy	10741	CAGTATTTTTATAAAACATTTCTTCACAACTCACACATTTTAAAAACAAAACACTGTCTC	10800
Db	10741	CAGTATTTTTATAAAACATTTCTTCACAACTCACACATTTTAAAAACAAAACACTGTCTC	10800
Qy	10801	TAAATCCCCAAATTTTTCATTAAC	10825
Db	10801	TAAATCCCCAAATTTTTCATTAAC	10825

Db 10801 TAAATCCCAAAATTTTTCATAAAC 10825

RESULT 9

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LOCUS AR036572 246240 bp DNA linear PAT 29-SEP-1999

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REFERENCE 1 (bases 1 to 246240)

AUTHORS Feder, J. Nathan., Kronmal, G. Scott., Lauer, P. M., Ruddy, D. A., Thomas, W., Tsuchihashi, Z., and Wolff, R. K.

TITLE Megabase transcript map: novel sequences and antibodies thereto

FEATURES

Location/Qualifiers

1..246240

/organism="unknown"

BASE COUNT 73211 a 50177 c 50599 g 72252 t 1 others

ORIGIN

Query Match 100.0%; Score 10823; DB 6; Length 246240;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCFAAGGTTGAGATAAAATTTTAAATGATGATCAATTTGAAATCATAAATATTTA 60

Db 192304 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTGAAATCATAAATATTTA 192363

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Db 192364 AATATCTAAAGTTTCAGATCAGACATTTGGAGCTACTTTTCCCAATCAACACACCCCT 192423

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Db 192424 TCAGGATTTTAAACCAAGGGGACACTGGATCACCCTAGTGTGTTTCAACAGCAGGTACCTT 192483

Qy 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCAACAGAACTT 240

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Qy 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGTGATCTCTGAGGCATCCCGC 300

Db 192544 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGTGATCTCTGAGGCATCCCGC 192603

Qy 301 TTTCCCGCCGCCCAAAAGAGCGAGATTTTAAAGGGAGCGTGGGCCAGAGCTGGGAA 360

Db 192604 TTTCCCGCCGCCCAAAAGAGCGAGATTTTAAAGGGAGCGTGGGCCAGAGCTGGGAA 192663

Qy 361 ATGGGCCCGAGCGAGCGCGGCTTCTCCTCTGATGCTTTTTCAGACACCGGTCCTG 420

Db 192664 ATGGGCCCGAGCGAGCGCGGCTTCTCCTCTGATGCTTTTTCAGACACCGGTCCTG 192723

Qy 421 CAGGGCGCTTGCTGGGTGAGTCCGAGGGTGGCGGCGAACTAGGGCGCGCGGGGGTG 480

Db 192724 CAGGGCGCTTGCTGGGTGAGTCCGAGGGTGGCGGCGAACTAGGGCGCGCGGGGTG 192783

Qy 481 GAAATTCGAATAGCTTTTCTTTTGGCTGGGAGTTGCTAACTTTGGAGACCTGC 540

Db 192784 GAAATTCGAATAGCTTTTCTTTTGGCTGGGAGTTGCTAACTTTGGAGACCTGC 192843

Qy 541 TCAACCCATCCGCAAGCCCTCTCCCTACTTTCTCGCTCCAGACCCCGTGAGGAGTGC 600

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Qy 601 CTACCACCTGAACCTGCAGATAGGGGTTCCTTCGCCCGCAGGACCTGCCCTTCCCGGGCTGT 560

Db 192904 CTACCACCTGAACCTGCAGATAGGGGTTCCTTCGCCCGCAGGACCTGCCCTTCCCGGGCTGT 192963

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Qy 1021 GGGAGGCTCCTGAGAGAGGCTACCTCGGCGCTTTTCCCACTCTTGGCAATTTGTTCTTTT 1080

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Qy 1081 GCCTGGAAAATTAAGTATATGTTAGTTTGAAGCTTTGAAGTGAAGTGAAGTGAAGTGA 1140

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Qy 1321 GGAATTCAGATTTATTAACCTTTTTCAGGTTTACAAGAACATAAATAAATCTGGTTTCTG 1380

Db 193624 GGAATTCAGATTTATTAACCTTTTTCAGGTTTACAAGAACATAAATAAATCTGGTTTCTG 193683

Qy 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTACGAGTGAATTTGGCCCTGTAG 1440

Db 193684 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTACGAGTGAATTTGGCCCTGTAG 193743

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Db 193984 AAATATTCATTTGTTTACAGTGAATTAAGTCCAGCCATGTGTTGCACCTGTTCAAGCCC 194043

Qy 1741 CAAGGGAGAGAGAGGAAACAAAGTCTTTACCCCTTTCATATTTTGCATTTCTAGTGGGAGA 1800

QY	3961	AGSGTGGGATCACATGTTCTCACTGTTGACCTCTTGGACTATTATGAAATACCAACCACAG	4020
Db	196264	AGSGTGGGATCACATGTTCTCACTGTTGACCTCTTGGACTATTATGAAATACCAACCACAG	196323
QY	4021	CAAGGTATGTGGAGAGGGGCGCTCACTTCCCTGAGGTGTGTGAGAGCTTTTTCATCTTTTC	4080
Db	196324	CAAGGTATGTGGAGAGGGGCGCTCACTTCCCTGAGGTGTGTGAGAGCTTTTTCATCTTTTC	196383
QY	4081	ATGCCATCTTGAAGGAACACCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAGAGGGAAG	4140
Db	196384	ATGCCATCTTGAAGGAACACCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAGAGGGAAG	196443
QY	4141	GAATTTCCTCCTCAGATCATTTTGGTCCCTTGGGGATGTTGGAATATAGGAGACCTATTCCCT	4200
Db	196444	GAATTTCCTCCTCAGATCATTTTGGTCCCTTGGGGATGTTGGAATATAGGAGACCTATTCCCT	196503
QY	4201	TGGTTGCAGTTTAAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCCTGCAGGTCACTC	4260
Db	196504	TGGTTGCAGTTTAAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCCCTGCAGGTCACTC	196563
QY	4261	GGCTGTGAANTGCBAAGAACACACGTACCGAGGGCTACTGGGAAGTACGGGTATGATGGG	4320
Db	196564	GGCTGTGAANTGCBAAGAACACACGTACCGAGGGCTACTGGGAAGTACGGGTATGATGGG	196623
QY	4321	CAGGACCACCTTGAATTCGCGCTGCACACTGGATTCGAGAGCAGCAGAACCCAGGGCC	4380
Db	196624	CAGGACCACCTTGAATTCGCGCTGCACACTGGATTCGAGAGCAGCAGAACCCAGGGCC	196683
QY	4381	TGGCCCCACCAAGCTGGAGTGGGAAGGCACAGANTCGGGCCAGGCAGACAGGGCCTAC	4440
Db	196684	TGGCCCCACCAAGCTGGAGTGGGAAGGCACAGANTCGGGCCAGGCAGACAGGGCCTAC	196743
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Db	196744	CTGGAGAGGGACTCCCTGTCACAGCTGCACAGTTGCTGGAGCTGGGGAGAGGTGTTTTG	196803
QY	4501	GACCAACAAAGTATGGTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG	4560
Db	196804	GACCAACAAAGTATGGTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG	196863
QY	4561	AGGTTGCAGGGCAGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCCTC	4620
Db	196864	AGGTTGCAGGGCAGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCCTC	196923
QY	4621	TCCAAATTCCTGGGAAGGACCTTCTCAATCCCTAGAGTCTACCTTATATTCAGATGTA	4680
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QY	4681	TGAGCAGGCCACAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA	4740
Db	196984	TGAGCAGGCCACAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA	197043
QY	4741	GTGCTCATGGCCCTTGCTTTTATTTAAACCAATATCTTTGTATTTATATACCTGTAA	4800
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QY	4801	AAATTTCAGAAATGTCAGGCCGGGCAGGTGGCTACCCCTGTATCCCGACCTTTGGG	4860
Db	197104	AAATTTCAGAAATGTCAGGCCGGGCAGGTGGCTACCCCTGTATCCCGACCTTTGGG	197163
QY	4861	AGCCGAGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAAGCCCTGACCAACATGTTGAA	4920
Db	197164	AGCCGAGCGGGTGGTCACAAGGTCAGGAGTTTGAGACCAAGCCCTGACCAACATGTTGAA	197223
QY	4921	ACCCGTCTCTAAAAATACAAAAATTAAGTGGTCACACTCATCGGACCTGTAGTCCCA	4980
Db	197224	ACCCGTCTCTAAAAATACAAAAATTAAGTGGTCACACTCATCGGACCTGTAGTCCCA	197283
QY	4981	GCTAATTCGAGGCTGAGGCAGGAGCATCGCTTGAACTGGGAGACGGAGATTCGACTGA	5040
Db	197284	GCTAATTCGAGGCTGAGGCAGGAGCATCGCTTGAACTGGGAGACGGAGATTCGACTGA	197343

QY	5041	GCCAAAGTCCGCCACTGC	ACTCCAGGCTAGGCAGAGT	GAGACTCCATCTTTAAAAA	5100	
Db	197344	GCCAAAGTCCGCCACTGC	ACTCCAGGCTAGGCAGAGT	GAGACTCCATCTTTAAAAA	197403	
QY	5101	AAAAA	AAAAAAGAAATTCAGAGAT	CTCAGCTATCATATGAATAC	CGACAAA	5160
Db	197404	AAAAA	AAAAAAGAAATTCAGAGAT	CTCAGCTATCATATGAATAC	CGACAAA	197463
QY	5161	ATATCAAGTGAAGGCAT	TTATCAGAGTAGAAGAA	TCCTTTTAGGTTAAAGTTT	CTTTTCAT	5220
Db	197464	ATATCAAGTGAAGGCAT	TTATCAGAGTAGAAGAA	TCCTTTTAGGTTAAAGTTT	CTTTTCAT	197523
QY	5221	AGAACATAGCAATATAC	TCTGAAGCTACCTATCTT	ACAAGTCGCGTCTCTTAT	AACAATGC	5280
Db	197524	AGAACATAGCAATATAC	TCTGAAGCTACCTATCTT	ACAAGTCGCGTCTCTTAT	AACAATGC	197583
QY	5281	CTCTTAGGTTGACCAAG	TGAACTGACCATCTGTAT	TCAATCATTTTCAATG	CACATAA	5340
Db	197584	CTCTTAGGTTGACCAAG	TGAACTGACCATCTGTAT	TCAATCATTTTCAATG	CACATAA	197643
QY	5341	AGGCAATTTTATCTAT	CAGAACAAAGAAATCGGT	TAACAGATATGTATATTT	TACATGTG	5400
Db	197644	AGGCAATTTTATCTAT	CAGAACAAAGAAATCGGT	TAACAGATATGTATATTT	TACATGTG	197703
QY	5401	AGGNAACRAGCTGATC	TGACTGCTCTCCAAGT	GACACTGTGTAGAGT	CCAATCTTAGG	5460
Db	197704	AGGNAACRAGCTGATC	TGACTGCTCTCCAAGT	GACACTGTGTAGAGT	CCAATCTTAGG	197763
QY	5461	ACACAAATGGTGTCTC	CTCTCTGAGCTGTGTTTT	TCTGAAAGGGTATTTCT	TCTCTCC	5520
Db	197764	ACACAAATGGTGTCTC	CTCTCTGAGCTGTGTTTT	TCTGAAAGGGTATTTCT	TCTCTCC	197823
QY	5521	AACCTATAGAAGAGT	GTGAAGTTCCAGTCTCT	CTCGCAAGGTTAAACAGAT	CCCCCTC	5580
Db	197824	AACCTATAGAAGAGT	GTGAAGTTCCAGTCTCT	CTCGCAAGGTTAAACAGAT	CCCCCTC	197883
QY	5581	CTCATCTCTCTCTTC	TCTGTCAAGTGCCTCTT	TGTTGAAGGTGACACAT	CATGTGACC	5640
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QY	5641	TCCTAGTGACCACTCT	ACGGTGTGGGCTTGAACT	TACTACCCCGAAGATCACC	ATG	5700
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QY	5701	AAGTGGCTGAAGGAT	TAAGCAGCCAAATGGAT	GCCAAAGGTTGCAACCT	TAAGAGCTATTG	5760
Db	198004	AAGTGGCTGAAGGAT	TAAGCAGCCAAATGGAT	GCCAAAGGTTGCAACCT	TAAGAGCTATTG	198063
QY	5761	CCCAATGGGATGGACCT	TACACGGGTGGATAACCT	TGTGGCTGTACCCCTTGGG	CAAGAG	5820
Db	198064	CCCAATGGGATGGACCT	TACACGGGTGGATAACCT	TGTGGCTGTACCCCTTGGG	CAAGAG	198123
QY	5821	CAGAGATATAGTNC	AGTGGAGGACCCAGGCT	TGGATCAGCCCTCATTTGT	GATCTGG	5880
Db	198124	CAGAGATATAGTNC	AGTGGAGGACCCAGGCT	TGGATCAGCCCTCATTTGT	GATCTGG	198183
QY	5881	GGTATGTGATCAT	GAGAGCCAGGAGTGTG	AGAAAATCTATTGGGGTGT	GAGAGAGTGCC	5940
Db	198184	GGTATGTGATCAT	GAGAGCCAGGAGTGTG	AGAAAATCTATTGGGGTGT	GAGAGAGTGCC	198243
QY	5941	TGAGGAGGTAAATTA	TGGCAGTGAGATGAG	GAATCTGCTTTTGTAGGGG	TGGGCTGAGG	6000
Db	198244	TGAGGAGGTAAATTA	TGGCAGTGAGATGAG	GAATCTGCTTTTGTAGGGG	TGGGCTGAGG	198303
QY	6001	GTGGCAATCAAGGCT	TTTAACCTTGTCTTTT	TCTGTATAGAGCCCTC	ACCGTCTGGCACCC	6060
Db	198304	GTGGCAATCAAGGCT	TTTAACCTTGTCTTTT	TCTGTATAGAGCCCTC	ACCGTCTGGCACCC	198363
QY	6061	TAGTCATTTGGAGTC	ATCAGTGGAAATGCTGT	TTTTGTGTCATCTTTGTC	ATTTGGAATTT	6120
Db	198364	TAGTCATTTGGAGTC	ATCAGTGGAAATGCTGT	TTTTGTGTCATCTTTGTC	ATTTGGAATTT	198423
QY	6121	TGTTTCATTAATTA	TAAAGGAAGGACGGG	TTTCAAGTGTAGGAACA	AAAGGGGAGTCTCT	6180

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Db 198424 TGTTCATAATATAAGGAAGAGCGAGGTCAAGTAGTAGGAACAAGGGGAAAGTCTCT 198483
QY 6181 TAGTACTCTGCCCGCCAGGCACAGTGGGAAGAGGGGCGAGAGGGGATCTGCCATCCATGGG 6240
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QY 6241 AAGCATTTTTCTCATTTATATCTTTTGGGGACACCAGCAGCTCCCTGGGAGACAGAAAAT 6300
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Db 198604 AATGGTCTCCCCCAGCAATGAAGTCTCTAATTCACAAAACATCTTCAGAGCACCTACTAT 198663
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QY 6541 ATCACATTGAGTGGGATCAGATAGCTCTCTGATCTTGAAGGAGAAGCTGGATTCCA 6600
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QY 6601 TTAGGTGAGGTTGAAGATGATGGGAGTCTACACAGACGGAGCAACCATGCCAAGTAGGA 6660
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Db 198964 GAGTATAAGGCATCTGGAGATTAAGAATAATTAATGTAACCTTGAACCTGAGTTGGCT 199023
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QY 6841 TCAGTGGGTGTATGAAGGATCTAAGAAAGGAGGACCAAGATCTCCCTTATATGGTG 6900
Db 199144 TCAGTGGGTGTATGAAGGATCTAAGAAAGGAGGACCAAGATCTCCCTTATATGGTG 199203
QY 6901 AATGCTCTCTTAAAGAGTTAGATGAGAGGTGAGGAGACCAAGTTAGAAGCCAAATAGCAT 6960
Db 199204 AATGCTCTCTTAAAGAGTTAGATGAGAGGTGAGGAGACCAAGTTAGAAGCCAAATAGCAT 199263
QY 6961 TTCCAGATCAGAGATAATGGTTCTTTGAATCCCAATAGTGCCCAAGGTCTAAATTCAGATGG 7020
Db 199264 TTCCAGATCAGAGATAATGGTTCTTTGAATCCCAATAGTGCCCAAGGTCTAAATTCAGATGG 199323
QY 7021 GTCAATGAGGAAATAGGAAGAGAGAGGCAAGATGGTCCCTAGGTTTGTGATGCCT 7080
Db 199324 GTCAATGAGGAAATAGGAAGAGAGAGGCAAGATGGTCCCTAGGTTTGTGATGCCT 199383
QY 7081 CTTTCTCGGTCTCTGTGTCACAGAGGAGCCATGGGCACTACGCTCTAGCTGAACG 7140
Db 199384 CTTTCTCGGTCTCTGTGTCACAGAGGAGCCATGGGCACTACGCTCTAGCTGAACG 199443
QY 7141 TGAGTCACAGCAGCTGCAGACTCACCTGTGGGAAGAGACAAAACCTAGAGACTCAAAGA 7200
Db 199444 TGAGTCACAGCAGCTGCAGACTCACCTGTGGGAAGAGACAAAACCTAGAGACTCAAAGA 199503
QY 7201 GGGAGTGCATTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGAACCTTAACATAGAAAT 7260
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Db 199504 GGGAGTGCATTTATGAGCTCTTTCATGTTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT 199563
QY 7261 GCCTGACGAACCTCTTGATTTTATAGCTTCTCTGTTCATTTCTCTCAAAAAGATTTCCCCAT 7320
Db 199564 GCCTGACGAACCTCTTGATTTTATAGCTTCTCTGTTCATTTCTCTCAAAAAGATTTCCCCAT 199623
QY 7321 TTAGGTTTCTGAGTTCTCTGCATGCCGGTGATCCCTPAGCTGTGACCTCTCCCTGGAACTG 7380
Db 199624 TTAGGTTTCTGAGTTCTCTGCATGCCGGTGATCCCTPAGCTGTGACCTCTCCCTGGAACTG 199683
QY 7381 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCTTCATTTCTCCTCCGTCACTCAGAG 7440
Db 199684 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCTTCATTTCTCCTCCGTCACTCAGAG 199743
QY 7441 ACATACACCTATGTCAATTTCAATTTCTTATTTTGAAGAGGACTCCTTTAAATTTGGGGGA 7500
Db 199744 ACATACACCTATGTCAATTTCAATTTCTTATTTTGAAGAGGACTCCTTTAAATTTGGGGGA 199803
QY 7501 CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCTTGGAGCTGGCTAGTCAT 7560
Db 199804 CTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCTTGGAGCTGGCTAGTCAT 199863
QY 7561 AACCTTACCAGATTTTACACATGATCTATGCAATTTTCTGGACCCGTTCACCTTTTCCT 7620
Db 199864 AACCTTACCAGATTTTACACATGATCTATGCAATTTTCTGGACCCGTTCACCTTTTCCT 199923
QY 7621 TTGAATCCTCTCTCTGTGTACCCAGTAACTCATCTGTCAACAAGCCCTTGGGGATTTCTC 7680
Db 199924 TTGAATCCTCTCTCTGTGTACCCAGTAACTCATCTGTCAACAAGCCCTTGGGGATTTCTC 199983
QY 7681 CATCTGATTTGATGAGTTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740
Db 199984 CATCTGATTTGATGAGTTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 200043
QY 7741 GCACCTGTCTCCAGAAAAGCATCATGGCTATCTGTGGTGTATGATGAGTGGTGTATTTAGC 7800
Db 200044 GCACCTGTCTCCAGAAAAGCATCATGGCTATCTGTGGTGTATGATGAGTGGTGTATTTAGC 200103
QY 7801 AGGTAGAGGCAAAATATCTTGAAGGGTTGTGAAGAGGTGTTTTTCTAATTTGGCATGA 7860
Db 200104 AGGTAGAGGCAAAATATCTTGAAGGGTTGTGAAGAGGTGTTTTTCTAATTTGGCATGA 200163
QY 7861 AGGTGTCAACAGATTTGCAAAAGTTTAAATGTCCTTCAATTTGGGATGCTACTAGTAT 7920
Db 200164 AGGTGTCAACAGATTTGCAAAAGTTTAAATGTCCTTCAATTTGGGATGCTACTAGTAT 200223
QY 7921 TCCAGACCTGAAGAATCACAATAATTTTCTAGCTGGTCTCTCTTGTCTGATTAATGAAA 7980
Db 200224 TCCAGACCTGAAGAATCACAATAATTTTCTAGCTGGTCTCTCTTGTCTGATTAATGAAA 200283
QY 7981 ATTATGATAGGATGATAAAGCACTTACTTCTGTCGGACTCTTCTGAGCACCCTACTTA 8040
Db 200284 ATTATGATAGGATGATAAAGCACTTACTTCTGTCGGACTCTTCTGAGCACCCTACTTA 200343
QY 8041 CATGCACTACTGCATGCATCTTACATAAATTTCTATGAGATGATGATTAATTTCCCAT 8100
Db 200344 CATGCACTACTGCATGCATCTTACATAAATTTCTATGAGATGATGATTAATTTCCCAT 200403
QY 8101 TTTCTTTTAAATGAAGAAGTGAAGTAGCGCGGACGGTGGCTCAGCGCTGTAAATCCC 8160
Db 200404 TTTCTTTTAAATGAAGAAGTGAAGTAGCGCGGACGGTGGCTCAGCGCTGTAAATCCC 200463
QY 8161 AGCACTTTGGGAGGCCAAAGCGGGTGGATCAGAGGTTCAGAGATTCAGAGACCATCTCTGGC 8220
Db 200464 AGCACTTTGGGAGGCCAAAGCGGGTGGATCAGAGGTTCAGAGATTCAGAGACCATCTCTGGC 200523
QY 8221 TAACATGGTGAACCCCACTCTCTAATAAAAATACAAAAATTTAGCTGGCGTGTGGCAG 8280
Db 200524 TAACATGGTGAACCCCACTCTCTAATAAAAATACAAAAATTTAGCTGGCGTGTGGCAG 200583
QY 8281 ACGCCTGTAGTCCCACTACTTGGAAAGGCTGAGGAGAGATGCGCATGAACCCAGAGG 8340
Db 200584 ACGCCTGTAGTCCCACTACTTGGAAAGGCTGAGGAGAGATGCGCATGAACCCAGAGG 200643
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QY	8341	CAGAGCTTGCAGT	GAGCCGAGTTTTGGCCACTGCAC	TCCAGCCTAGGTGACAGAGTGAGA	8400
Db	200644				
		CAGAGCTTGCAGT	GAGCCGAGTTTTGGCCACTGCAC	TCCAGCCTAGGTGACAGAGTGAGA	200703
QY	8401	CTCCATCTCAAAAAA	TAAAAATAAAAATAAAAAATGAAAAA	AAAAAGAAAGTGAAGTA	8460
Db	200704	CTCCATCTCAAAAAA	TAAAAATAAAAATAAAAAATGAAAAA	AAAAAGAAAGTGAAGTA	200763
QY	8461	TAGAGTATCTCAT	AGTTGTGCAGTGATAGAACAGGTTTCAAA	ACTCAGTCAATCTGACCG	8520
Db	200764	TAGAGTATCTCAT	AGTTGTGCAGTGATAGAACAGGTTTCAAA	ACTCAGTCAATCTGACCG	200823
QY	8521	TTTGATACATCT	CAGACACCACTACATCAGTAGTTAGAT	GCGCTAGATAAATACAGAA	8580
Db	200824	TTTGATACATCT	CAGACACCACTACATCAGTAGTTAGAT	GCGCTAGATAAATACAGAA	200883
QY	8581	GGAAGGAGATGGCT	TCTTCTCTGTCTCATTTGTGTTTCTTCT	GAGTGAGCTTGAATCACAT	8640
Db	200884	GGAAGGAGATGGCT	TCTTCTCTGTCTCATTTGTGTTTCTTCT	GAGTGAGCTTGAATCACAT	200943
QY	8641	GAGGGGAACAGC	AGAAAAACCACTGATCTCAGCTCTCAT	GTTTCCCTTTAAAAAGTC	8700
Db	200944	GAGGGGAACAGC	AGAAAAACCACTGATCTCAGCTCTCAT	GTTTCCCTTTAAAAAGTC	201003
QY	8701	CCTGAAGGAAGGTC	TGSAATGTCACTCCCTTGCCTCTCTCT	CTGTCCTCTTTGGCATTTCA	8760
Db	201004	CCTGAAGGAAGGTC	TGSAATGTCACTCCCTTGCCTCTCTCT	CTGTCCTCTTTGGCATTTCA	201063
QY	8761	TTTCTTTTGGACCC	TACGCAAGGACTGTAATTGGTGGGACAGCT	AGTGGCCCTGCTGGGC	8820
Db	201064	TTTCTTTTGGACCC	TACGCAAGGACTGTAATTGGTGGGACAGCT	AGTGGCCCTGCTGGGC	201123
QY	8821	TTACACACAGGTG	TCTCCCTTAGCCAGTGCCTCTGGAGTCAGAACT	CTGTTGGTATTTTC	8880
Db	201124	TTACACACAGGTG	TCTCCCTTAGCCAGTGCCTCTGGAGTCAGAACT	CTGTTGGTATTTTC	201183
QY	8881	CCTCAATGAAGT	GAGTAAGTCTCTCATTTTGAGATGGTAT	TAATGGAAGCCACCAGTGC	8940
Db	201184	CCTCAATGAAGT	GAGTAAGTCTCTCATTTTGAGATGGTAT	TAATGGAAGCCACCAGTGC	201243
QY	8941	GCTTAGAGGATG	CCCCAGGTCTTCCATGGAGCCACTGGGT	TCCGGTGCACATTAATAAAA	9000
Db	201244	GCTTAGAGGATG	CCCCAGGTCTTCCATGGAGCCACTGGGT	TCCGGTGCACATTAATAAAA	201303
QY	9001	AAAACTAACAG	AGACATTTCAGGAATTCGTAGATTC	TGGGAAATCAGTTCAACCATGTTCA	9060
Db	201304	AAAACTAACAG	AGACATTTCAGGAATTCGTAGATTC	TGGGAAATCAGTTCAACCATGTTCA	201363
QY	9061	AAAGAGCTTTT	TTTTTTTTTTTGTAGACTCTATTGCC	CAGGCTGGAGTGCATGGCATGAT	9120
Db	201364	AAAGAGCTTTT	TTTTTTTTTTTGTAGACTCTATTGCC	CAGGCTGGAGTGCATGGCATGAT	201423
QY	9121	CTCGGCTCACT	GTAAACCTCTGCCTCCAGGTTCAAGCGA	TTCTCCTGTCTCAGCCCTCCCA	9180
Db	201424	CTCGGCTCACT	GTAAACCTCTGCCTCCAGGTTCAAGCGA	TTCTCCTGTCTCAGCCCTCCCA	201483
QY	9181	AGTAGCTGGGA	TATACAGGCGTGACCACCATGCTCCG	CGGCTAAATTTTGTATTTTAGTAGA	9240
Db	201484	AGTAGCTGGGA	TATACAGGCGTGACCACCATGCTCCG	CGGCTAAATTTTGTATTTTAGTAGA	201543
QY	9241	GACAGGTTTT	CACCATGTTGGCCAGGCTGGTCTCGAACT	CTCCTGACCTCGTGATCCCGC	9300
Db	201544	GACAGGTTTT	CACCATGTTGGCCAGGCTGGTCTCGAACT	CTCCTGACCTCGTGATCCCGC	201603
QY	9301	TGCCTCGGCCT	CCCAAGTGTCTGAGATTCACAGGTGT	GAGCCACCCCTGCCACGCCGTCAA	9360
Db	201604	TGCCTCGGCCT	CCCAAGTGTCTGAGATTCACAGGTGT	GAGCCACCCCTGCCACGCCGTCAA	201663
QY	9361	AGAGCTCTTA	TATATATATCCAGATGGCATGTGTTT	ACTTTATGTTACTACATGCACTTG	9420
Db	201664	AGAGCTCTTA	TATATATATCCAGATGGCATGTGTTT	ACTTTATGTTACTACATGCACTTG	201723

QY	9421	GCTGCTAAATGTGGTACAAGCATCTGCTTTGAAGGCGCAGGTGCTTCAGGATAACCATAT	9480
Db	201724	GCTGCTAAATGTGGTACAAGCATCTGCTTTGAAGGCGCAGGTGCTTCAGGATAACCATAT	201783
QY	9481	ACAGCTCAGAAGTTCTCTCTTTAGGCATTTAAATTTAGCAAAAGATATCTCATCTCTCTTT	9540
Db	201784	ACAGCTCAGAAGTTCTCTCTTTAGGCATTTAAATTTAGCAAAAGATATCTCATCTCTCTTT	201843
QY	9541	TTAAACCAATTTCTTTTTTTTGTGTTAGAAAGTTATGTAGAAAAAGTAAATGTGATTT	9600
Db	201844	TTAAACCAATTTCTTTTTTTTGTGTTAGAAAGTTATGTAGAAAAAGTAAATGTGATTT	201903
QY	9601	AGGCTCATGTAGAAAAAGCTATAAAATGAATACAAATTTAAAGCTGTTATTTAATTAGCCAG	9660
Db	201904	AGGCTCATGTAGAAAAAGCTATAAAATGAATACAAATTTAAAGCTGTTATTTAATTAGCCAG	201963
QY	9661	TGAAAAACTATTAACAACCTGTCTATTACCTGTTAGTATTATTGTTGCATTTAAAAATGCA	9720
Db	201964	TGAAAAACTATTAACAACCTGTCTATTACCTGTTAGTATTATTGTTGCATTTAAAAATGCA	202023
QY	9721	TATACCTTTAAATAATGTATTTGTTATGTTATCTGCAATGATTTTATTTGAAGTTCTTGTTTC	9780
Db	202024	TATACCTTTAAATAATGTATTTGTTATGTTATCTGCAATGATTTTATTTGAAGTTCTTGTTTC	202083
QY	9781	AFCTTGTGTATATACTTAATCGCTTGTCATTTTGGAGACAATTAATTTGCTTCTAATTT	9840
Db	202084	ATCTTGTGTATATACTTAATCGCTTGTCATTTTGGAGACAATTAATTTGCTTCTAATTT	202143
QY	9841	CTTTACATTTTGTCTTAGGNAATATTTTCATTTCAACTGTTGGTAGCCGAATTAATCGTGT	9900
Db	202144	CTTTACATTTTGTCTTAGGNAATATTTTCATTTCAACTGTTGGTAGCCGAATTAATCGTGT	202203
QY	9901	TCTTCACCTTAGGGACATTTGTCGCTAAAGTTGTAAGACATTTGGTTATTTTACCAGCAAAAC	9960
Db	202204	TCTTCACCTTAGGGACATTTGTCGCTAAAGTTGTAAGACATTTGGTTATTTTACCAGCAAAAC	202263
QY	9961	CATCTGAAAGCATATGACAAATTTATTTCTCTCTTAATATCTTACTATATACTGAAAGCAGA	10020
Db	202264	CATCTGAAAGCATATGACAAATTTATTTCTCTCTTAATATCTTACTATATACTGAAAGCAGA	202323
QY	10021	CTGCTATAAGGCTTTCACCTTACTCTTACCTCATAGGAATATGTTACAAATTAATTTAT	10080
Db	202324	CTGCTATAAGGCTTTCACCTTACTCTTACCTCATAGGAATATGTTACAAATTAATTTAT	202383
QY	10081	AGGTAAGCATTTGTTTATATTTGGTTTATTTCCACCTGGCTCAGATTTTCAAGAAACACC	10140
Db	202384	AGGTAAGCATTTGTTTATATTTGGTTTATTTCCACCTGGCTCAGATTTTCAAGAAACACC	202443
QY	10141	CCAGTCTTCAGTAAACACATTTTCACTAACACATTTACTAAACATCAGCAACTGTGGCT	10200
Db	202444	CCAGTCTTCAGTAAACACATTTTCACTAACACATTTACTAAACATCAGCAACTGTGGCT	202503
QY	10201	GTTAAATTTTAAATAGAAATTTTAAAGTCTCATTTTCTTCGGTGTGTTTTTAAAGTTAA	10260
Db	202504	GTTAAATTTTAAATAGAAATTTTAAAGTCTCATTTTCTTCGGTGTGTTTTTAAAGTTAA	202563
QY	10261	TTTTTCTGGCTTTATTCATAAAATTTCTTAAAGTCAACTACATTTTGAAGAAATCAAGACCTG	10320
Db	202564	TTTTTCTGGCTTTATTCATAAAATTTCTTAAAGTCAACTACATTTTGAAGAAATCAAGACCTG	202623
QY	10321	CATTTTAAATTTCTTATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAA	10380
Db	202624	CATTTTAAATTTCTTATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAA	202683
QY	10381	GGGTGACACCTGGTGGCCATAGGTAAATGTACACCGTGGTCCGGTGACCGAGATGCAG	10440
Db	202684	GGGTGACACCTGGTGGCCATAGGTAAATGTACACCGTGGTCCGGTGACCGAGATGCAG	202743
QY	10441	CGCTGAGGGTTTTCTCAAGGTAAAGGAATAAAGATGGTGGAGGGGCGTGCACCTGGA	10500
Db	202744	CGCTGAGGGTTTTCTCAAGGTAAAGGAATAAAGATGGTGGAGGGGCGTGCACCTGGA	202803
QY	10501	ATCACTTGTAGAGAAAAAGCCCTGAAATTTTGAGAAAAACAAACAGAAACTTCTTACCAG	10560

Qy	1441	TGTAGCAGAGTGTCTGTGGGTACACCGCGGCTCAGCACAGCACTTTGAGTTTTGGTA	1500
Db	193744	TGTAGCAGAGTGTCTGTGGGTACACCGCGGCTCAGCACAGCACTTTGAGTTTTGGTA	193803
Qy	1501	CTAGCTGTATCCACATTTTACATATGACAAGATGAGGCATGCACGGCTGCTCCTCG	1560
Db	193804	CTAGCTGTATCCACATTTTACATATGACAAGATGAGGCATGCACGGCTGCTCCTCG	193863
Qy	1561	CAAAATTTATCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATAGC	1620
Db	193864	CAAAATTTATCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATAGC	193923
Qy	1621	TATGATTTTAAACATCACACTGCATTAGAGTTTGAATATAAATTTTCAATGTTGAGCAG	1680
Db	193924	TATGATTTTAAACATCACACTGCATTAGAGTTTGAATATAAATTTTCAATGTTGAGCAG	193983
Qy	1681	AAATATTCAATGTTTCAAGTGTAAATGAGTCCACAGCATGTGTGCACGTGTTCAAGCCC	1740
Db	193984	AAATATTCAATGTTTCAAGTGTAAATGAGTCCACAGCATGTGTGCACGTGTTCAAGCCC	194043
Qy	1741	CAAGGGAGAGCAGCAGGGAAACAAGTCTTTTACCCTTTTGATATTTTGCAATTTCTAGTGGGAGA	1800
Db	194044	CAAGGGAGAGCAGCAGGGAAACAAGTCTTTTACCCTTTTGATATTTTGCAATTTCTAGTGGGAGA	194103
Qy	1801	GATGACAATATAGCAAAATGACGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA	1860
Db	194104	GATGACAATATAGCAAAATGACGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA	194163
Qy	1861	GAACACAGAGAGTCAGGCAAGTCACHTCGGGCTGACACTTGACAGAGACATGNAAGA	1920
Db	194164	GAACACAGAGAGTCAGGCAAGTCACHTCGGGCTGACACTTGACAGAGACATGNAAGA	194223
Qy	1921	AATAAGAAATGATATTGACTGGGAGCAGTATTTCCACAGGCAAACTGAGTGGGCTGCGCAAG	1980
Db	194224	AATAAGAAATGATATTGACTGGGAGCAGTATTTCCACAGGCAAACTGAGTGGGCTGCGCAAG	194283
Qy	1981	TTGGATTTAAAGCGGGTTTTCTCAGCACHACTCATGTGTGTGTGTGGGGGGGGGG	2040
Db	194284	TTGGATTTAAAGCGGGTTTTCTCAGCACHACTCATGTGTGTGTGTGGGGGGGGGG	194343
Qy	2041	CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTAGCATATCTCTGT	2100
Db	194344	CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTAGCATATCTCTGT	194403
Qy	2101	CCTCCCTACTCACTAGTGTAGGAGCACHCCCCCAGTCTTGACAAACCAAAATGTCTCT	2160
Db	194404	CCTCCCTACTCACTAGTGTAGGAGCACHCCCCCAGTCTTGACAAACCAAAATGTCTCT	194463
Qy	2161	AAACTTTGCCACATGTCACTAGTAGACAAACTTCCTGGTTTAAAGAGCTCGGGTTGAAAA	2220
Db	194464	AAACTTTGCCACATGTCACTAGTAGACAAACTTCCTGGTTTAAAGAGCTCGGGTTGAAAA	194523
Qy	2221	AATAAACAGTAGTGTGGGAGTCAGGCAAGAGTAGGTAAATGGGCTCAGAGAGGA	2280
Db	194524	AATAAACAGTAGTGTGGGAGTCAGGCAAGAGTAGGTAAATGGGCTCAGAGAGGA	194583
Qy	2281	GCCACAAACAGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATTTCTAGCCAAAGGAGTA	2340
Db	194584	GCCACAAACAGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATTTCTAGCCAAAGGAGTA	194643
Qy	2341	ACAGTGATCTGCACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGAAAGCAGAGATG	2400
Db	194644	ACAGTGATCTGCACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGAAAGCAGAGATG	194703
Qy	2401	AAGGGACACAGTAAAGCAGGGAGCCACGACGAGAGCTGTTACACAGTCCAGGCAG	2460
Db	194704	AAGGGACACAGTAAAGCAGGGAGCCACGACGAGAGCTGTTACACAGTCCAGGCAG	194763
Qy	2461	AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAAGGAGTGACAAAACTTTGTCCTCTGAA	2520
Db	194764	AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAAGGAGTGACAAAACTTTGTCCTCTGAA	194823
Qy	2521	TATATTTGAAAGAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAAAGAGATTTGG	2580

Db	194824	TATATCTGAAGAGAGTTGCTGAAGAGATTCTATGTTGTCGAGAGAAAGAGAATTTGG	194883
QY	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGCAGACAGATTCCTGAGCTCAGGA	2640
Db	194884	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGCAGACAGATTCCTGAGCTCAGGA	194943
QY	2641	GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTCTCAAAAAATACAAAAATTA	2700
Db	194944	GTTCAAGACCAGCCTGGGCAACACAGCAAAACCCCTTCTCTCAAAAAATACAAAAATTA	195003
QY	2701	GCTGGGTGTGGATGCGACTGTGATCCTAGCTACTCGGAGGCTGAGGTGGAGGTA	2760
Db	195004	GCTGGGTGTGGATGCGACTGTGATCCTAGCTACTCGGAGGCTGAGGTGGAGGTA	195063
QY	2761	TGTGTTGAGCCAGGAGTTGAGCTCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820
Db	195064	TGTGTTGAGCCAGGAGTTGAGCTCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	195123
QY	2821	CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGACTTAAAGT	2880
Db	195124	CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGACTTAAAGT	195183
QY	2881	TGACTTTGTTCTTATTTTAAATTTATTTGSCCTGAGCAGTGGGGTAAATCAAGATCTGCATTTG	2940
Db	195184	TGACTTTGTTCTTATTTTAAATTTATTTGSCCTGAGCAGTGGGGTAAATCAAGATCTGCATTTG	195243
QY	2941	TCTCGAGATGCTGAAGCAGAGGAAAGACAGAGTTGGGGTAAATCAAGATCTGCATTTG	3000
Db	195244	TCTCGAGATGCTGAAGCAGAGGAAAGACAGAGTTGGGGTAAATCAAGATCTGCATTTG	195303
QY	3001	GGACATGTTAAGTTTGAGATTCCAGTTCAGGCTTCCAGTGGTGAGGCCACATAGGCAGTT	3060
Db	195304	GGACATGTTAAGTTTGAGATTCCAGTTCAGGCTTCCAGTGGTGAGGCCACATAGGCAGTT	195363
QY	3061	CAGTGTAGAATTCAGGACCAAGGCTGGGCAAGGCTGGCTCAGTTCCTGATATCCAGCACT	3120
Db	195364	CAGTGTAGAATTCAGGACCAAGGCTGGGCAAGGCTGGCTCAGTTCCTGATATCCAGCACT	195423
QY	3121	TTGTTGGCTGAGGAGGATGAGATCATTTGAGTCAAGGAGTTTGAGACAAGCTTGCGCAACA	3180
Db	195424	TTGTTGGCTGAGGAGGATGAGATCATTTGAGTCAAGGAGTTTGAGACAAGCTTGCGCAACA	195483
QY	3181	TGGTGAACCCCATCTCTACTAAAAATACAAAAATTTAGCCTGGTGGTGCGCAGCCCT	3240
Db	195484	TGGTGAACCCCATCTCTACTAAAAATACAAAAATTTAGCCTGGTGGTGCGCAGCCCT	195543
QY	3241	ATAGTCCAGGTTTTCAGGAGGCTTAGGTAGGAGATTCCTTTGAACCCAGGAGGTGCAGG	3300
Db	195544	ATAGTCCAGGTTTTCAGGAGGCTTAGGTAGGAGATTCCTTTGAACCCAGGAGGTGCAGG	195603
QY	3301	TTGCAGTCAGCTGAGATTTGTCGCACTCCACTCCAGCTGGGTGATAGAGTGAGACTTGT	3360
Db	195604	TTGCAGTCAGCTGAGATTTGTCGCACTCCACTCCAGCTGGGTGATAGAGTGAGACTTGT	195663
QY	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAATGAAAGAAATTTATTCCTCAGGATTTGGG	3420
Db	195664	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAATGAAAGAAATTTATTCCTCAGGATTTGGG	195723
QY	3421	TCTAATTTGGCCCTGAGCACCACCTCCTGAGTTCACTTACCATGGCTAGACACACCTTAAC	3480
Db	195724	TCTAATTTGGCCCTGAGCACCACCTCCTGAGTTCACTTACCATGGCTAGACACACCTTAAC	195783
QY	3481	ATTTTCTTAGAATTCACACAGCTTTAGTGCGATCTGTCTAATCATGAGTATTTGGAATAGAT	3540
Db	195784	ATTTTCTTAGAATTCACACAGCTTTAGTGCGATCTGTCTAATCATGAGTATTTGGAATAGAT	195843
QY	3541	CTGGGGCAGTGAGGGGTTGCGACCCAGCTGTCGACAGAAAAAGCACAAAGAAAGCC	3600
Db	195844	CTGGGGCAGTGAGGGGTTGCGACCCAGCTGTCGACAGAAAAAGCACAAAGAAAGCC	195903
QY	3601	ACCCAGGACTGTATATGGAAGAAAGACAGGACTGCAACTTCACCCCTTCACAAATCAGGA	3660

Db 195904 ACCGAGACTGTCATATGGGAAGAAACACAGGACTGCAACTCACCCCTTCACAAAATGAGGA 195963
 Qy 3661 CCAGACACAGCTGATGGTATGAGTTGATGACAGGTGTGTGAGGCTCAACATCTCTGCTCC 3720
 Db 195964 CCAGACACAGCTGATGGTATGAGTTGATGACAGGTGTGTGAGGCTCAACATCTCTGCTCC 196023
 Qy 3721 CTCTACTACACATGGTTAAGGCTGTGTCTGTCTCCAGGTTACACTCTCTGACACTA 3780
 Db 196024 CTCTACTACACATGGTTAAGGCTGTGTCTGTCTCCAGGTTACACTCTCTGACACTA 196083
 Qy 3781 CTTCTTCATGGGTGCTTCAGACAGAGACCTTGGTCTTTCTCTGTTTGAAGCTTTTGGGCTA 3840
 Db 196084 CTTCTTCATGGGTGCTTCAGACAGAGACCTTGGTCTTTCTCTGTTTGAAGCTTTTGGGCTA 196143
 Qy 3841 CGTGGATGACAGCTGTCTGTCTTATGATNATGAGAGTCGCCGTGTGGAGCCCGGAAC 3900
 Db 196144 CGTGGATGACAGCTGTCTGTCTTATGATCATGAGAGTCGCCGTGTGGAGCCCGGAAC 196203
 Qy 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA 3960
 Db 196204 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA 196263
 Qy 3961 AGGTGGGATACATGTTCAGTCTGTGACTTCTGACTATTATGAAAAATCAACAACACAG 4020
 Db 196264 AGGTGGGATACATGTTCAGTCTGTGACTTCTGACTATTATGAAAAATCAACAACACAG 196323
 Qy 4021 CAAGGGTATGTGAGAGGGGCCCTCACCTTCCTGAGGTTGTTCAGAGCTTTTCACTTTTC 4080
 Db 196324 CAAGGGTATGTGAGAGGGGCCCTCACCTTCCTGAGGTTGTTCAGAGCTTTTCACTTTTC 196383
 Qy 4081 ATGCATCTCAAGGAACACAGCTGGAAGTCTGAGGCTTGTGGAGCAGGAAGAGGGAAG 4140
 Db 196384 ATGCATCTCAAGGAACACAGCTGGAAGTCTGAGGCTTGTGGAGCAGGAAGAGGGAAG 196443
 Qy 4141 GAATTTCTCTCCTGAGATCATTTGGTCTTTGGGATGGTGGAAATAGGACCTATTCCCTT 4200
 Db 196444 GAATTTCTCTCCTGAGATCATTTGGTCTTTGGGATGGTGGAAATAGGACCTATTCCCTT 196503
 Qy 4201 TGGTTGAGTTTACAGAGCTGGGGATTTTTCAGAGTCCACACCCTGAGGTCATCCCTG 4260
 Db 196504 TGGTTGAGTTTACAGAGCTGGGGATTTTTCAGAGTCCACACCCTGAGGTCATCCCTG 196563
 Qy 4261 GGCTGTCAATGCAAGAAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG 4320
 Db 196564 GGCTGTGAATGCAAGAAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG 196623
 Qy 4321 CAGGACCACCTTGAATTTCTGCCCTGACACACTGGATTTGGAGACAGACACCAGGGCC 4380
 Db 196624 CAGGACCACCTTGAATTTCTGCCCTGACACACTGGATTTGGAGACAGACACCAGGGCC 196683
 Qy 4381 TGGCCCAACCAAGCTGGAGTGGGAAGGCACAAGATTTCGGGCCAGGACAGAGGGCTAC 4440
 Db 196684 TGGCCCAACCAAGCTGGAGTGGGAAGGCACAAGATTTCGGGCCAGGACAGAGGGCTAC 196743
 Qy 4441 CTGGAGAGGACTGCCCTGACACAGCTCAGCAGTTGCTGGAGCTGGGAGAGGTGTTTG 4500
 Db 196744 CTGGAGAGGACTGCCCTGACACAGCTCAGCAGTTGCTGGAGCTGGGAGAGGTGTTTG 196803
 Qy 4501 GACCAACAAGGTATGTTGGAAACACACTTCTGCCCTTATCTACTAGTGGCAGAGTGGAGG 4560
 Db 196804 GACCAACAAGGTATGTTGGAAACACACTTCTGCCCTTATCTACTAGTGGCAGAGTGGAGG 196863
 Qy 4561 AGGTTGAGGCGACCGAATCCCTGGTTGGAGTTTCAGAGTGGCTGAGGCTGTGCTCCTC 4620
 Db 196864 AGGTTGAGGCGACCGAATCCCTGGTTGGAGTTTCAGAGTGGCTGAGGCTGTGCTCCTC 196923
 Qy 4621 TCCAAATTCCTGGGAAGGACTTTCTCAATCCTAGAGTCTCTACTTATATTCAGATGTA 4680
 Db 196924 TCCAAATTCCTGGGAAGGACTTTCTCAATCCTAGAGTCTCTACTTATATTCAGATGTA 196983
 Qy 4681 TGAGACGCCACAAAGTATGGGTTTAAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA 4740
 Db 196984 TGAGACGCCACAAAGTATGGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAGGGAA 197043

Qy 4741 GTGTCTATGGCCCTGCTTTTATTTTAAACCAATAATCTTTTGTATATTTATACCTGTATA 4800
 Db 197044 GTGTCTATGGCCCTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTATA 197103
 Qy 4801 AAATTCAGAAATGTCAAGCCGGGCACGGTGCCTCACCCCTGTAATCCCAGCACTTTGGG 4860
 Db 197104 AAATTCAGAAATGTCAAGCCGGGCACGGTGCCTCACCCCTGTAATCCCAGCACTTTGGG 197163
 Qy 4861 AGGCCGAGCGGGTGGTCACAAAGGTACAGAGTTTGAGACCAGCCTGACCAACATCGTGAA 4920
 Db 197164 AGGCCGAGCGGGTGGTCACAAAGGTACAGAGTTTGAGACCAGCCTGACCAACATCGTGAA 197223
 Qy 4921 ACCCGTCTCTAAAAAATACAAAAATTAAGCTGGTCACAGTCATCGGCACCTGTAGTCCCA 4980
 Db 197224 ACCCGTCTCTAAAAAATACAAAAATTAAGCTGGTCACAGTCATCGGCACCTGTAGTCCCA 197283
 Qy 4981 GCTAATTCGAAGGCTGAGCGAGGAGCATCGCTTGAACCTGGGAAGCGAAGTTGCACCTGA 5040
 Db 197284 GCTAATTCGAAGGCTGAGCGAGGAGCATCGCTTGAACCTGGGAAGCGAAGTTGCACCTGA 197343
 Qy 5041 GCCAAGATCGCGCCACTGCACCTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTTAAAAA 5100
 Db 197344 GCCAAGATCGCGCCACTGCACCTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTTAAAAA 197403
 Qy 5101 AAAAAAAGGAGAGATTCAGAGATCTCAGCTATCATATGATATGATATGATATGATATGAT 5160
 Db 197404 AAAAAAAGGAGAGATTCAGAGATCTCAGCTATCATATGATATGATATGATATGATATGAT 197463
 Qy 5161 ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCCTTTAGGTTAAAAAGTTCTTTTCAT 5220
 Db 197464 ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCCTTTAGGTTAAAAAGTTCTTTTCAT 197523
 Qy 5221 AGAACATAGCAATATACCTGAAGTACCTATCTTTACAAAGTCCCGTCTTTATACAAATGC 5280
 Db 197524 AGAACATAGCAATATACCTGAAGTACCTATCTTTACAAAGTCCCGTCTTTATACAAATGC 197583
 Qy 5281 CTCCTTAGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGACACATA 5340
 Db 197584 CTCCTTAGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGACACATA 197643
 Qy 5341 AGGCAATTTTATCTATCAGAACAAAGAACATGGGTAACAGATATGATATTTACATGTG 5400
 Db 197644 AGGCAATTTTATCTATCAGAACAAAGAACATGGGTAACAGATATGATATTTACATGTG 197703
 Qy 5401 AGGAGAACAGCTGATCTGACTGCTCTCCAGTGACACTGTGTAGAGTCCAACTTTAGG 5460
 Db 197704 AGGAGAACAGCTGATCTGACTGCTCTCCAGTGACACTGTGTAGAGTCCAACTTTAGG 197763
 Qy 5461 ACACAAAATGGTGTCTCTCCTGTAGCTTTGTTTTCTGAAAAGGATTTTCTCTCCTCC 5520
 Db 197764 ACACAAAATGGTGTCTCTCCTGTAGCTTTGTTTTCTGAAAAGGATTTTCTCTCCTCC 197823
 Qy 5521 AACCTATAGAAAGAGTGAAGTTCCAGTCTTCTTGGCAAGGGTAAACAGATCCCTCTC 5580
 Db 197824 AACCTATAGAAAGAGTGAAGTTCCAGTCTTCTTGGCAAGGGTAAACAGATCCCTCTC 197883
 Qy 5581 CTCATCTCTCTCTTTCTCTGTCAGTGCCCTCTTTTGGTGAAGGTGACACATCATGTGACC 5640
 Db 197884 CTCATCTCTCTCTTTCTCTGTCAGTGCCCTCTTTTGGTGAAGGTGACACATCATGTGACC 197943
 Qy 5641 TCTTCAGTGACCACTCTACGGTGTGGGCTTGAACCTACTACCCCGACAAATCACCATTG 5700
 Db 197944 TCTTCAGTGACCACTCTACGGTGTGGGCTTGAACCTACTACCCCGACAAATCACCATTG 198003
 Qy 5701 AAGTGGCTCAAGGATTAAGCAGCAATGGATGCCAAGAGGTTTGAACCTTAAAGACGTAATG 5760
 Db 198004 AAGTGGCTCAAGGATTAAGCAGCAATGGATGCCAAGAGGTTTGAACCTTAAAGACGTAATG 198063
 Qy 5761 CCCAATGGGGATGGGACCTACAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAG 5820
 Db 198064 CCCAATGGGGATGGGACCTACAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAG 198123

QY	5821	CAGAGATACGTCNCAGGTGGAGCACCCAGCGCTGGATCGATCAGCCCTCATTTGTATCTGG	5880
Db	198124	CAGAGATACGTCGCCAGGTGGAGCACCCAGCGCTGGATCAGCCCTCATTTGTATCTGG	198183
QY	5881	GGTATGCTGACTCATCAGAGCCAGGAGCTGAGAAAATCTATTTGGGGGTTGAGAGAGTGC	5940
Db	198184	GGTATGTGACTGATCAGAGCCAGGAGCTGAGAAAATCTATTTGGGGGTTGAGAGAGTGC	198243
QY	5941	TGAGGAGGTAAATTATGCGACTGAGATCAGATCTGCTCTTTGTTTAGGGGGTGGCTGAGG	6000
Db	198244	TGAGGAGGTAAATTATGCGACTGAGATCAGATCTGCTCTTTGTTTAGGGGGTGGGCTGAGG	198303
QY	6001	GTGGCAATCAAGGCTTTAACTTGCTTTTCTGTTTATAGACCCCTCACCGCTCTGGCACCC	6060
Db	198304	GTGGCAATCAAGGCTTTAACTTGCTTTTCTGTTTATAGACCCCTCACCGCTCTGGCACCC	198363
QY	6061	TAGTCATTTGGGAGTCATCAGTGGAAATTCGTCGTTTGTGTCGTCATCTTGTTCATTTGGAATTT	6120
Db	198364	TAGTCATTTGGGAGTCATCAGTGGAAATTCGTCGTTTGTGTCGTCATCTTGTTCATTTGGAATTT	198423
QY	6121	TGTTCATATAATTAAGGAAGAGCCAGGGTTCAAGTCACTAGTAAACAAGGGGGAAGTCTCT	6180
Db	198424	TGTTCATATAATTAAGGAAGAGCCAGGGTTCAAGTCACTAGTAAACAAGGGGGAAGTCTCT	198483
QY	6181	TAGTACCTCTGCCCGAGGACAGTGGGAAGAGGGGCAGAGGGATCTGCATCCATGGG	6240
Db	198484	TAGTACCTCTGCCCGAGGACAGTGGGAAGAGGGGCAGAGGGATCTGCATCCATGGG	198543
QY	6241	AAGCATTTTCTCATAATTAATCTTTTGGGACACCAAGCAGCTCCCTGGGAGACAGAAAAAT	6300
Db	198544	AAGCATTTTCTCATAATTAATCTTTTGGGACACCAAGCAGCTCCCTGGGAGACAGAAAAAT	198603
QY	6301	AATGGTTCTCCCGAGAATGAAGTCTTAATTCACAACAACATCTTCAGAGCACTACTAT	6360
Db	198604	AATGGTTCTCCCGAGAATGAAGTCTTAATTCACAACAACATCTTCAGAGCACTACTAT	198663
QY	6361	TTTGCACAGAGCTGTTTAAGTGTAGTACAGGGGCTTTGAGGTTGAGAGTCACTCTGGGCTAT	6420
Db	198664	TTTGCACAGAGCTGTTTAAGTGTAGTACAGGGGCTTTGAGGTTGAGAGTCACTCTGGGCTAT	198723
QY	6421	TCTCAGAACCCAAATCTGGTAGGGAATGAAATGTATAGCAAGTAAATGTAGTTAAAGAAAG	6480
Db	198724	TCTCAGAACCCAAATCTGGTAGGGAATGAAATGTATAGCAAGTAAATGTAGTTAAAGAAAG	198783
QY	6481	ACCCATGAGGTCTTAAAGCAGGCGAGGAACAAATGCTTTAGGGTGTCAAGAGGAAGAAATG	6540
Db	198784	ACCCATGAGGTCTTAAAGCAGGCGAGGAACAAATGCTTTAGGGTGTCAAGAGGAAGAAATG	198843
QY	6541	ATCATTACAGCTGGGATCAAGATAGCCTTCTGGATCTTCAAGGAGAAAGCTGGATTCCA	6600
Db	198844	ATCATTACAGCTGGGATCAAGATAGCCTTCTGGATCTTCAAGGAGAAAGCTGGATTCCA	198903
QY	6601	TTAGTGTAGGTGAGATGATGGGAGTCTACACAGAGGGAGCAACCATGCCAAGTAGGA	6660
Db	198904	TTAGTGTAGGTGAGATGATGGGAGTCTACACAGAGGGAGCAACCATGCCAAGTAGGA	198963
QY	6661	GAGTATAGGCATACCTGGAGATTAGAAATTAATTACTGTACCTTAACCCCTGAGTTTCGCT	6720
Db	198964	GAGTATAGGCATACCTGGAGATTAGAAATTAATTACTGTACCTTAACCCCTGAGTTTCGCT	199023
QY	6721	AGCTATCACTACCAAAATTATGCATTTCTACCCCTTGACATCTGTGGTGTAGGGAAAGA	6780
Db	199024	AGCTATCACTACCAAAATTATGCATTTCTACCCCTTGACATCTGTGGTGTAGGGAAAGA	199083
QY	6781	GAATCAGAAGAAGCCAGCTCATACAGAGTCCAAGGGCTTTTGGGATATTGGGTTATGA	6840
Db	199084	GAATCAGAAGAAGCCAGCTCATACAGAGTCCAAGGGCTTTTGGGATATTGGGTTATGA	199143
QY	6841	TCAGTGGGTGTCAATTGAGGATCCTTAAGAAAGGAGGACCAAGATCTCCCTTATATGGTG	6900
Db	199144	TCAGTGGGTGTCAATTGAGGATCCTTAAGAAAGGAGGACCAAGATCTCCCTTATATGGTG	199203
QY	6901	AATGTGTTGTTTAAGAAAGTTAGATGAGAGTGTAGGAGACCAAGTTAGAAAGGCCAATTAAGCAT	6960

Db	199204	AATCTGTGTTTAAAGAGTTAGATGAGAGGTGAGGAGACCAAGTTAGAAAGCCAAATAAGCAT	199263
Qy	6961	TTCCAGATGAGAGATAATGGTCTTGTGAAATCCCAATAGTGCCAGGTCTAAATTTGAGATGG	7020
Db	199264	TTCCAGATGAGAGATAATGGTCTTGTGAAATCCCAATAGTGCCAGGTCTAAATTTGAGATGG	199323
Qy	7021	GTGAATGAGGAAATAAGGAAGAGAGAGAGGCAAGATGGTGCTTAGTTTGTGATGGCT	7080
Db	199324	GTGAATGAGGAAATAAGGAAGAGAGAGAGGCAAGATGGTGCTTAGTTTGTGATGGCT	199383
Qy	7081	CTTTCCCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGCACTAGCTCTTAGCTGAAGC	7140
Db	199384	CTTTCCCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGCACTAGCTCTTAGCTGAAGC	199443
Qy	7141	TGAGTGACAGCCGCTCGACAGCTCACTGTGGGAAGGAGACAAACTAGAGACTCAAGA	7200
Db	199444	TGAGTGACAGCCGCTCGACAGCTCACTGTGGGAAGGAGACAAACTAGAGACTCAAGA	199503
Qy	7201	GGGAGTGCAATTAATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT	7260
Db	199504	GGGAGTGCAATTAATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT	199563
Qy	7261	GCCTGAGCAACTCCTTGATTTTAGCCCTTCCTGTCATTTCCCAAAAAGATTTCCCCAT	7320
Db	199564	GCCTGAGCAACTCCTTGATTTTAGCCCTTCCTGTCATTTCCCAAAAAGATTTCCCCAT	199623
Qy	7321	TTAGGTTCTGAGTTTCTGCATGCGCGGTGATTCCTAGCTGTGACCTCTCCCTGGGAAGTG	7380
Db	199624	TTAGGTTTCTGAGTTTCTGCATGCGCGGTGATTCCTAGCTGTGACCTCTCCCTGGGAAGTG	199683
Qy	7381	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCCTCCGTCACCTCAGAG	7440
Db	199684	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCCTCCGTCACCTCAGAG	199743
Qy	7441	ACATACACCTATGTCATTTTCATTTTCTTATTTTGGAGAGAGGACTCCTTAAATTTGGGGGA	7500
Db	199744	ACATACACCTATGTCATTTTCATTTTCTTATTTTGGAGAGAGGACTCCTTAAATTTGGGGGA	199803
Qy	7501	CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTTGAACCCCTGGGACGTGGCTAGTCAT	7560
Db	199804	CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTTGAACCCCTGGGACGTGGCTAGTCAT	199863
Qy	7561	AACCTTACCAGATTTTACACATGATCTATGATTTTCTGAGCCGCTCAACTTTTCCT	7620
Db	199864	AACCTTACCAGATTTTACACATGATCTATGATTTTCTGAGCCGCTCAACTTTTCCT	199923
Qy	7621	TTGAATCCTCTCTCTGTGTTTACCAGTAACCTCATCTGTCAACAGCCTTGGGATTTCTTC	7680
Db	199924	TTGAATCCTCTCTCTGTGTTTACCAGTAACCTCATCTGTCAACAGCCTTGGGATTTCTTC	199983
Qy	7681	CATCTGATGCGATCTGATGTCACAGCTATGAGCGTGTACACTGCACGAATGGAAGAG	7740
Db	199984	CATCTGATGCGATCTGATGTCACAGCTATGAGCGTGTACACTGCACGAATGGAAGAG	200043
Qy	7741	GCACCTCTCCACAGAAAAGCATATGCTATCTGTGGGTAGTAGTGGGTGTTTTAGC	7800
Db	200044	GCACCTCTCCACAGAAAAGCATATGCTATCTGTGGGTAGTAGTGGGTGTTTTAGC	200103
Qy	7801	AGGTAGGAGGCCAATATCTTCAAAAGGGTCTGAGAGGTTGTTTTTCTAATTTGGCATGA	7860
Db	200104	AGGTAGGAGGCCAATATCTTCAAAAGGGTCTGAGAGGTTGTTTTTCTAATTTGGCATGA	200163
Qy	7861	AGGTGTCATACAGATTTGCAAGTTTAAATGGTGCTTCAATTTGGGATGCTACTAGTAT	7920
Db	200164	AGGTGTCATACAGATTTGCAAGTTTAAATGGTGCTTCAATTTGGGATGCTACTAGTAT	200223
Qy	7921	TCCAGACCTGAAGAAATCACATAATTTTCTACCTGGTCTCTCCTGTGTCGATGAATGAAA	7980
Db	200224	TCCAGACCTGAAGAAATCACATAATTTTCTACCTGGTCTCTCCTGTGTCGATGAATGAAA	200283
Qy	7981	ATTATGAAGGATGATAAAGACATTACTTCGTGTCGCCGACTCTCTCTGAGCACCTACTTA	8040

Db 200284 ATTATGATAGGATGATAAAGCACATTACTTGGTCCGACCTCTTCTGAGCACCTACTTA 200343
Qy 8041 CATGCATTACTGCATGCACCTTCTTACAATAATTCATGAGATAGGTACTATTATCCCCAT 8100
Db 200344 CATGCATTACTGCATGCACCTTCTTACAATAATTCATGAGATAGGTACTATTATCCCCAT 200403
Qy 8101 TTCTTTTAAATGAAGAAAGTGAAGTGAAGCGGACGGTGGCTCAGCGCTCTAATCCC 8160
Db 200404 TTCTTTTAAATGAAGAAAGTGAAGTGAAGCGGACGGTGGCTCAGCGCTCTAATCCC 200463
Qy 8161 AGCACTTTGGAGGCCAAAGCGGTGATCAGCAGGTTCAGGAGATCGAGACCATCTCTGGC 8220
Db 200464 AGCACTTTGGAGGCCAAAGCGGTGATCAGCAGGTTCAGGAGATCGAGACCATCTCTGGC 200523
Qy 8221 TAACATGGTGAACCCCATCTCTAATAAAAATACAAAAATTAGCTGGGCGTGGTGGCAG 8280
Db 200524 TAACATGGTGAACCCCATCTCTAATAAAAATACAAAAATTAGCTGGGCGTGGTGGCAG 200583
Qy 8281 ACGCCTGTAGTCCAGCTACTCGGAAGGCTGAGCGAGGAATGGCATGAACCCAGGAGG 8340
Db 200584 ACGCCTGTAGTCCAGCTACTCGGAAGGCTGAGCGAGGAATGGCATGAACCCAGGAGG 200643
Qy 8341 CAGAGCTTGCAGTGAGCGGAGTTTTCGCCACTGCACCTCCAGCCTTAGGTGACAGAGTGAGA 8400
Db 200644 CAGAGCTTGCAGTGAGCGGAGTTTTCGCCACTGCACCTCCAGCCTTAGGTGACAGAGTGAGA 200703
Qy 8401 CTCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 8460
Db 200704 CTCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 200763
Qy 8461 TAGAGTATCTCATAGTTGTGCAGTGATAGAACAGGTTTCAAACTCAGTCAATCTGACCG 8520
Db 200764 TAGAGTATCTCATAGTTGTGCAGTGATAGAACAGGTTTCAAACTCAGTCAATCTGACCG 200823
Qy 8521 TTTGATACATCTCAGACACCACACTACATTCAGTAGTTAGATGCCCTAGATAAATAAGAGAA 8580
Db 200824 TTTGATACATCTCAGACACCACACTACATTCAGTAGTTAGATGCCCTAGATAAATAAGAGAA 200883
Qy 8581 GGAAGGAGATGGCTTCTCTTTGTCTCATTTGTGTTTCTTCTGAGTGAGCTTGAATCACAT 8640
Db 200884 GGAAGGAGATGGCTTCTCTTTGTCTCATTTGTGTTTCTTCTGAGTGAGCTTGAATCACAT 200943
Qy 8641 GAAGGGAAACAGCAGAAAAACCAACTGATCCTCAGCTGTCACTGTTTCCCTTTAAAAAGTC 8700
Db 200944 GAAGGGAAACAGCAGAAAAACCAACTGATCCTCAGCTGTCACTGTTTCCCTTTAAAAAGTC 201003
Qy 8701 CCTGAAGGAAGTCCCTGGAATGTGACTCCCTTGCTCCCTCTGTTGCTCTCTTTGGCATTTCA 8760
Db 201004 CCTGAAGGAAGTCCCTGGAATGTGACTCCCTTGCTCCCTCTGTTGCTCTCTTTGGCATTTCA 201063
Qy 8761 TTCTCTTTGGACCCCTACGGAAGACTGTAAATTTGGTGGGACAGCTAGTGGCCCTCTGGGC 8820
Db 201064 TTCTCTTTGGACCCCTACGGAAGACTGTAAATTTGGTGGGACAGCTAGTGGCCCTCTGGGC 201123
Qy 8821 TTTCACACGGGTGCTCCTCCTAGGCGAGTGCCTCTGAGTGCAGAACTCTGGTGGTATTTC 8880
Db 201124 TTTCACACGGGTGCTCCTCCTAGGCGAGTGCCTCTGAGTGCAGAACTCTGGTGGTATTTC 201183
Qy 8881 CCTCAATGAAGTGGAGTAGTCTCTCTCAATTTTGAGATGGTATAATGGAAGCCACCAAGTG 8940
Db 201184 CCTCAATGAAGTGGAGTAGTCTCTCTCAATTTTGAGATGGTATAATGGAAGCCACCAAGTG 201243
Qy 8941 GCTTAGAGGATGCCAGGTCTCTTCAATGGAGCCACTGGGGTCCGGTGCACATTAATAAAA 9000
Db 201244 GCTTAGAGGATGCCAGGTCTCTTCAATGGAGCCACTGGGGTCCGGTGCACATTAATAAAA 201303
Qy 9001 AAAATCTACAGGACATTCAGGAATTCAGATTCGGAATTCAGGAACTCAGTTCACCATGTTC 9060
Db 201304 AAAATCTACAGGACATTCAGGAATTCAGATTCGGAATTCAGGAACTCAGTTCACCATGTTC 201363
Qy 9061 AAAGAGTCTTT 9120
Db 201364 AAAGAGTCTTT 201423

Qy 9121 CTCGGCTCAGCTGAACCTCTGCCTCCAGGTTCAAGCGAHTTCTCCTGTCTCAGCCTCCCA 9180
Db 201424 CTCGGCTCAGCTGAACCTCTGCCTCCAGGTTCAAGCGAHTTCTCCTGTCTCAGCCTCCCA 201483
Qy 9181 AGTAGCTGGGATTACAGCGGTGACCCACCATCGCCGGGTAAATTTTGTATTTTAGTAGA 9240
Db 201484 AGTAGCTGGGATTACAGCGGTGACCCACCATCGCCGGGTAAATTTTGTATTTTAGTAGA 201543
Qy 9241 GACAGGGTTTCACCATGTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 9300
Db 201544 GACAGGGTTTCACCATGTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCC 201603
Qy 9301 TGCCTCGGCCCTCCCAAAAGTGTGAGATTACAGGTGTGAGCCACCCCTGCCAGCCGTCAAA 9360
Db 201604 TGCCTCGGCCCTCCCAAAAGTGTGAGATTACAGGTGTGAGCCACCCCTGCCAGCCGTCAAA 201663
Qy 9361 AGAGCTTTAAT 9420
Db 201664 AGAGCTTTAAT 201723
Qy 9421 GCTGCATAAATCTGTTACAGCATTCGTCTGGAAGGCGAGGTCTTCAGGATACCATAT 9480
Db 201724 GCTGCATAAATCTGTTACAGCATTCGTCTGGAAGGCGAGGTCTTCAGGATACCATAT 201783
Qy 9481 ACAGCTCAGAAGTTTCTTCTTTAGGCATTTAAATTTAGCAAAAGATATCTCATCTCTTCT 9540
Db 201784 ACAGCTCAGAAGTTTCTTCTTTAGGCATTTAAATTTAGCAAAAGATATCTCATCTCTTCT 201843
Qy 9541 TTAACACATTTCTTTTTTTTGGTTAGAAAAGTTATGTAGAAAAAGTAATGTGATTT 9600
Db 201844 TTAACACATTTCTTTTTTTTGGTTAGAAAAGTTATGTAGAAAAAGTAATGTGATTT 201903
Qy 9601 ACCTCATTTGTAGAAAGCTATAAAATGAATACAATTAAGCTGTTATTAATTAAGCCAG 9660
Db 201904 ACCTCATTTGTAGAAAGCTATAAAATGAATACAATTAAGCTGTTATTAATTAAGCCAG 201963
Qy 9661 TGAAGAACTATTAAACAACTTGTCTATTACCTGTAGTATTATTGTGTGCATTTAAAAATGCA 9720
Db 201964 TGAAGAACTATTAAACAACTTGTCTATTACCTGTAGTATTATTGTGTGCATTTAAAAATGCA 202023
Qy 9721 TATACCTTTAATAATGTATATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 9780
Db 202024 TATACCTTTAATAATGTATATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 202083
Qy 9781 ATCTTGATATATACCTTAATCGCTTTGTCAATTTTGGAGACATTTATTTGCTCTTAATTT 9840
Db 202084 ATCTTGATATATACCTTAATCGCTTTGTCAATTTTGGAGACATTTATTTGCTCTTAATTT 202143
Qy 9841 CTTTACATTTTGTCTTACGGAATATTTTCAATCAACTGGTGAAGCGAATTAATCGTGT 9900
Db 202144 CTTTACATTTTGTCTTACGGAATATTTTCAATCAACTGGTGAAGCGAATTAATCGTGT 202203
Qy 9901 TCTTCACTCTAGGACATTTGCTCTAAAGTTGTAAGACATTTGGTTATTTTACCAGCAAC 9960
Db 202204 TCTTCACTCTAGGACATTTGCTCTAAAGTTGTAAGACATTTGGTTATTTTACCAGCAAC 202263
Qy 9961 CATTTGAAAGCATATGACAAATTTTCTCTCTTAATATCTTACTATACTGAAAGCAGA 10020
Db 202264 CATTTGAAAGCATATGACAAATTTTCTCTCTTAATATCTTACTATACTGAAAGCAGA 202323
Qy 10021 CTGCTATAAGGCTTCACTTACTCTTCTTACCTCATTAAGGAATATGTTACAAATTAATTTAT 10080
Db 202324 CTGCTATAAGGCTTCACTTACTCTTCTTACCTCATTAAGGAATATGTTACAAATTAATTTAT 202383
Qy 10081 AGGTAAGCATTTGTTTATATTTGTTTTTATTTTACCTGGGCTGAGATTTCAAGAAACACC 10140
Db 202384 AGGTAAGCATTTGTTTATATTTGTTTTTATTTTACCTGGGCTGAGATTTCAAGAAACACC 202443
Qy 10141 CCAGTCTTCAGTAACACATTTTCACTAACACATTTTACTAAACATACAGCACTGTGGCCT 10200
Db 202444 CCAGTCTTCAGTAACACATTTTCACTAACACATTTTACTAAACATACAGCACTGTGGCCT 202503

QY 5521 AACCTATAGAAAGAGCTGAAAGTTCCAGTCTTCCCTGGCAAGGGTAAACAGATCCCCCTCTC 5580
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Db 197824 AACCTATAGAAAGAGTGAAGGTTCCAGTCTTCCCTGGCAAGGGTAAACAGATCCCCCTCTC 197883
QY 5581 CTCATCCTTCCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC 5640
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Db 197884 CTCATCCTTCCCTCTTTCCTGTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC 197943
QY 5641 TCTTCAGTGACCCTCTACGGTGTGGGGCTTGAACCTACTACCCCGAGAACATCACCATG 5700
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Db 197944 TCTTCAGTGACCCTCTACGGTGTGGGGCTTGAACCTACTACCCCGAGAACATCACCATG 198003
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Db 198004 AAGTGGCTGAAGGATAGAGCAACATGAGTGCACAGAGCTTGAACCTAAAGACGTAATG 198063
QY 5761 CCCAATGGGATGGGACCTACCAAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG 5820
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Db 198064 CCCAATGGGATGGGACCTACCAAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG 198123
QY 5821 CAGAGATATACGTTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTGATCTGG 5880
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QY 5881 GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGGTTGAGAGGAGTGCC 5940
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QY 6121 TGTTCATTAATTAAGCAAGCAGCGGTTCAAGTAGTAGGAACAAAGGGGGAAGTCTCT 6180
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Db 198664 TTTGCAAGAGCTGTTTAAAGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 198723
QY 6421 TCTCAGAACCCAAATCTGGTGAAGGAATGAATTCATAGCAAGTAATTCATAGTTAAAGAG 6480
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Db 198724 TCTCAGAACCCAAATCTGGTGAAGGAATGAATTCATAGCAAGTAATTCATAGTTAAAGAG 198783
QY 6481 ACCCATCAGCTCCTAAAGCAGGACGAGCAAAATGCTTAGGGTGTCAAAGGAAGAAATG 6540
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Db 198784 ACCCATCAGCTCCTAAAGCAGGACGAGCAAAATGCTTAGGGTGTCAAAGGAAGAAATG 198843
QY 6541 ATCATTTCAGCTGGGGATCAAGATAGCCCTTCTGGATCTTTGAAGGAGAAGCTGGATTTCCA 6600
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Db 198844 ATCATTTCAGCTGGGGATCAAGATAGCCCTTCTGGATCTTTGAAGGAGAAGCTGGATTTCCA 198903

QY 6601 TTAGTGAGGTTGAAGATGATGGAGGCTTACACAGAGGAGCAACCATCCCAAGTAGGA 6660
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Db 198904 TTAGTGAGGTTGAAGATGATGGAGGCTTACACAGAGGAGCAACCATCCCAAGTAGGA 198963
QY 6661 GAGTATAGGCATACTCGGAGATTAGAAATAATTACTGTACCTTAAACCCCTGAGTTTGCCT 6720
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Db 198964 GAGTATAGGCATACTCGGAGATTAGAAATAATTACTGTACCTTAAACCCCTGAGTTTGCCT 199023
QY 6721 AGCTATCAGTCAACCAATATATGCATTTCTACCCCTGAACATCTGTGTGTAGGGAAGA 6780
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QY 6781 GAATCAGAAAGAGCCAGCTCATACAGATCCAAGGCTCTTTGGGATATTGGTTATGA 6840
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QY 6841 TCACCTGGGCTGTCAATTGAAGGATCCTAAGAAAGGAGGACCAACGATCTCCCTTATATGGTG 6900
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Db 199144 TCACCTGGGCTGTCAATTGAAGGATCCTAAGAAAGGAGGACCAACGATCTCCCTTATATGGTG 199203
QY 6901 AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGCCAGTTAGAAAGCCAAATAAGCAT 6960
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Db 199204 AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGCCAGTTAGAAAGCCAAATAAGCAT 199263
QY 6961 TTCAGATGAGAGATATGTTCTTGAATCCAATAGTCCCAAGTCTTAATTTGAGATGG 7020
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Db 199264 TTCAGATGAGAGATATGTTCTTGAATCCAATAGTCCCAAGTCTTAATTTGAGATGG 199323
QY 7021 GTGAATGAGGAAAATAAGAAAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCC 7080
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Db 199324 GTGAATGAGGAAAATAAGAAAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCC 199383
QY 7081 CTTTCCCTGGGCTCTTGTCTCCACAGGAGGAGCCATGGGGCACTACGCTTTAGCTGAACG 7140
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Db 199384 CTTTCCCTGGGCTCTTGTCTCCACAGGAGGAGCCATGGGGCACTACGCTTTAGCTGAACG 199443
QY 7141 TGAGTGACACGAGCCTGCAGACTCACCTGTGGGAAGGAGACAAACCTAGAGACTCAAAGA 7200
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QY 7201 GGGAGTGCAATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATGAAT 7260
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QY 7261 GCCTGACGAACTCCTGATTTAGCTTCTCTGTTCAATTTCTCCTCAAAAAGATTTCCCAT 7320
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QY 7321 TTAGGTTTCTGAGTTCCCTGATGCCGCTGATCCCTAGCTGTGACCTCTCCCTGGAACTG 7380
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QY 7381 TCTCTCAGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCATTTCTCCGTCACTCAGAG 7440
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Db 199684 TCTCTCAGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCATTTCTCCGTCACTCAGAG 199743
QY 7441 ACATACACCTATGTCATTTTCATTTCTTATTTTGAAGAGGACTCCTTAAATTTTGGGGA 7500
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Db 199744 ACATACACCTATGTCATTTTCATTTCTTATTTTGAAGAGGACTCCTTAAATTTTGGGGA 199803
QY 7501 CTTTACATGATTTTAAACATCTGAGAAAAGCTTTGAACCCCTGGGAGCTGGCTAGTCA 7560
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Db 199804 CTTTACATGATTTTAAACATCTGAGAAAAGCTTTGAACCCCTGGGAGCTGGCTAGTCA 199863
QY 7561 AACCTTACAGATTTTACACATGATTCATGATTTTCTGGACCCGTTCAACTTTTCTCT 7620
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Db 199864 AACCTTACAGATTTTACACATGATTCATGATTTTCTGGACCCGTTCAACTTTTCTCT 199923
QY 7621 TTGAATCTCTCTCTGTTTACCCAGTAATCATCTGTCCACCAAGCTTGGGGATTTCTTC 7680
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Db 199924 TTGAATCTCTCTCTGTTTACCCAGTAATCATCTGTCCACCAAGCTTGGGGATTTCTTC 199983
QY 7681 CATCTGATTTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGAAGAG 7740

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Db 19984 CATCTGATTGTGATGTGAGTTGCACAGCTATGAAGCCTCTACACTGCAGAAATGAAGAG 200043
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Db 200044 GCACCTGTCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTAGC 200103
Qy 7801 AGGTAGGAGCAAAATATCTTGAAGGGGTGTGAAGAGGTGTTTTTCTTAATTTGGCATGA 7860
Db 200104 AGGTAGGAGCAAAATATCTTGAAGGGGTGTGAAGAGGTGTTTTTCTTAATTTGGCATGA 200163
Qy 7861 AGGTGTACATAGATTTGCAAGTTTAAATGGTGCCCTTCATTTGGGATGCTACTCTAGTAT 7920
Db 200164 AGGTGTACATAGATTTGCAAGTTTAAATGGTGCCCTTCATTTGGGATGCTACTCTAGTAT 200223
Qy 7921 TCCAGACCTTGAAGATACAAATAATTTTCTACCTGGTCTCTCCCTGTGTTCTGATAATGAAA 7980
Db 200224 TCCAGACCTTGAAGATACAAATAATTTTCTACCTGGTCTCTCCCTGTGTTCTGATAATGAAA 200283
Qy 7981 ATTATGATAAGGATGATAAAAGCACCTTACTTGGTCCGACTCTTCTGAGCACCTACTTGA 8040
Db 200284 ATTATGATAAGGATGATAAAAGCACCTTACTTGGTCCGACTCTTCTGAGCACCTACTTGA 200343
Qy 8041 CATGCAATFACTGCACTCTCTTACAATAATCTATGAGATAGTACTATTTATCCCAT 8100
Db 200344 CATGCAATFACTGCACTCTCTTACAATAATCTATGAGATAGTACTATTTATCCCAT 200403
Qy 8101 TTCTTTTTTAAATGAAGAAAGTGAAGTAGGCGCGGCAGGTGGCTACGCGCTGTAATCCC 8160
Db 200404 TTCTTTTTTAAATGAAGAAAGTGAAGTAGGCGCGGCAGGTGGCTACGCGCTGTAATCCC 200463
Qy 8161 AGCACTTTGGGAGGCCAAGCGGGTGGATCAGAGGTGAGGATCGAGACCATCTGGC 8220
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Qy 8221 TAACATGTTGAACCCCATCTCTATATAAATACAAAAATTAAGTGGCGTGGTGGCAG 8280
Db 200524 TAACATGTTGAACCCCATCTCTATATAAATACAAAAATTAAGTGGCGTGGTGGCAG 200583
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Qy 8341 CAGAGCTTCGAGTGAGCCGAGTTTGGCCACTGCACCTCCAGCCTAGGTGACAGAGTGAGA 8400
Db 200644 CAGAGCTTCGAGTGAGCCGAGTTTGGCCACTGCACCTCCAGCCTAGGTGACAGAGTGAGA 200703
Qy 8401 CTCACATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8460
Db 200704 CTCACATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 200763
Qy 8461 TAGAGTATCTCATAGTTTGTCTAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG 8520
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Qy 8521 TTTGATACATCTCAGACACCATACATTCAGTAGTATTTAGATGCCCTAGAGTAAATAGAGAA 8580
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Qy 8581 GGAAGAGATGCGTCT 8640
Db 200884 GGAAGAGATGCGTCT 200943
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Qy 8761 TTTCTTTGGACCCCTACGCAAGGACTGTAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGC 8820
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Qy 8821 TTCAACACACGGTGTCTCTCCCTAGCCAGTCCCTCTGGAGTCAGAACTCTCTGGTGGTATTTC 8880
Db 201124 TTCAACACACGGTGTCTCTCCCTAGCCAGTCCCTCTGGAGTCAGAACTCTCTGGTGGTATTTC 201183
Qy 8881 CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGGATGTGTATTAATGAAGCCACCAAGTG 8940
Db 201184 CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGGATGTGTATTAATGAAGCCACCAAGTG 201243
Qy 8941 GCTTAGAGGATGCCAGGTCCTTCCATGGAGCCACTGGGGTCCGGTGGACATTAATAAAA 9000
Db 201244 GCTTAGAGGATGCCAGGTCCTTCCATGGAGCCACTGGGGTCCGGTGGACATTAATAAAA 201303
Qy 9001 AAAATCTAAACAGGACATTCAGGAATTCGTAGATTTCTGGAAATCAGTTCACCATGTTC 9060
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Qy 9061 AAAGAGTCTTTTTTTTTTTTTTTTGGAGACTTATTGCCAGGCTGGAGTGCATGGCATGAT 9120
Db 201364 AAAGAGTCTTTTTTTTTTTTTTTTGGAGACTTATTGCCAGGCTGGAGTGCATGGCATGAT 201423
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Db 201424 CTCGGCTCACTGAACCTCTGCTCCAGGTTCAAGCGATTCCTGTCTCAGCCTCCCA 201483
Qy 9181 AGTAGCTGGGATTACAGCGCTGCACCACCATGCCCGCTAAATTTTGTATTTTAGTAGA 9240
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Qy 9241 GACAGGTTTTCAACATGTTGGCCAGGCTGCTCTCGAACTCTCTCTGACCTCGTATCCGCC 9300
Db 201544 GACAGGTTTTCAACATGTTGGCCAGGCTGCTCTCGAACTCTCTCTGACCTCGTATCCGCC 201603
Qy 9301 TGCTCTCGGCTCCCAAGTCTGAGATTACAGGTTCAGCGACCCCTGCCAGCCGCTCAA 9360
Db 201604 TGCTCTCGGCTCCCAAGTCTGAGATTACAGGTTCAGCGACCCCTGCCAGCCGCTCAA 201663
Qy 9361 AGAGCTTAATATATATATATCCAGATGCGATGTTACTTTACTTACTACTACATGCAATAT 9420
Db 201664 AGAGCTTAATATATATATCCAGATGCGATGTTACTTTACTTTACTACTACATGCAATAT 201723
Qy 9421 GCTGCATAAATGGGTCAAGCATCTCTTGAAGGCGAGGTCTTCAGGATACCATAT 9480
Db 201724 GCTGCATAAATGGGTCAAGCATCTCTTGAAGGCGAGGTCTTCAGGATACCATAT 201783
Qy 9481 ACAGCTCAGAGTTTCTCTTTAGGCATTAATTTTAGCAAAAGATATCTCATCTCTCTT 9540
Db 201784 ACAGCTCAGAGTTTCTCTTTAGGCATTAATTTTAGCAAAAGATATCTCATCTCTCTT 201843
Qy 9541 TTAACACATTTCTTTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 9600
Db 201844 TTAACACATTTCTTTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 201903
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Qy 9781 ATCTTGTATATACTTAATCGCTTTTGTCAATTTTGGAGACATTTATTTTCTCTTAATTT 9840
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Qy 9841 CTTTACATTTTGTCTTACGGAATATTTTCACTCAACTGTGGTGGTCCGCAATTAATCGTGT 9900
Db 202144 CTTTACATTTTGTCTTACGGAATATTTTCACTCAACTGTGGTGGTCCGCAATTAATCGTGT 202203
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Qy	9901	TCCTCACTCTAGGACATTCGCTCTAAGCTGTGAACACATTCGTTATTTACCAGCAAC	9960	SOURCE	human.
Db	202204	TCCTCACTCTAGGACATTCGCTCTAAGCTGTGAACACATTCGTTATTTACCAGCAAC	202263	ORGANISM	Homo sapiens
Qy	9961	CATTCTGAAAGCATATGACAAATATTTCTCTCTAATCTTACTATATCTACTGAAAGCAGA	10020	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	202264	CATTCTGAAAGCATATGACAAATATTTCTCTCTAATCTTACTATATCTACTGAAAGCAGA	202323	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Qy	10021	CTGCTATAAGGCTTCACTTACTCTTCTACCTCATAGGAATATGTTACAAATTAATTTATT	10080	TITLE	1 (bases 1 to 858)
Db	202324	CTGCTATAAGGCTTCACTTACTCTTCTACCTCATAGGAATATGTTACAAATTAATTTATT	202383	JOURNAL	Albig, W., Drabent, B., Burmester, N., Bode, C. and Doenecke, D.
Qy	10081	AGGTAAAGCATTTCTTATATTTGGTTTATTTTCACCTGGGCTGAGATTTCAAGAAACACC	10140	MEDLINE	The haemochromatosis candidate gene HFE (HLA-H) of man and mouse is
Db	202384	AGGTAAAGCATTTCTTATATTTGGTTTATTTTCACCTGGGCTGAGATTTCAAGAAACACC	202443	REFERENCE	located in syntenic regions within the histone gene cluster
Qy	10141	CCAGTCTTCAAGTAAACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTGGCCT	10200	AUTHORS	J. Cell. Biochem. 69 (2), 117-126 (1998)
Db	202444	CCAGTCTTCAAGTAAACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTGGCCT	202503	TITLE	2 (bases 1 to 12146)
Qy	10201	GTTAAATTTTTTAAATAGAAATTTAAGTCTCTCATTTTCTTCGGTGTTTTTTAAGCTTAA	10260	JOURNAL	Albig, W.
Db	202504	GTTAAATTTTTTAAATAGAAATTTAAGTCTCTCATTTTCTTCGGTGTTTTTTAAGCTTAA	202563	TITLE	Direct Submission
Qy	10261	TTTTTCTGGCTTTATTCATAAATTTCTTAAGTCAACTACATTTGAAAATCAAGACCTG	10320	JOURNAL	Submitted (14-MAR-1997) Albig W., Georg-August-Universitaet
Db	202564	TTTTTCTGGCTTTATTCATAAATTTCTTAAGTCAACTACATTTGAAAATCAAGACCTG	202623	REFERENCE	Goettingen, Biochemie und Molekulare Zellbiologie, Humboldtallee
Qy	10321	CATTTTAAATTTCTTATTCACCTCTGGCAAAACCATTTCAAAAACCATGGTAGTAAAGAGAA	10380	FEATURES	Location/Qualifiers
Db	202624	CATTTTAAATTTCTTATTCACCTCTGGCAAAACCATTTCAAAAACCATGGTAGTAAAGAGAA	202683	source	1. 12146
Qy	10381	GGGTGACACCTGTGGCCATAGTAATGTACCACGGTGGTCCGGTGACACAGATGCAG	10440	exon	/organism="Homo sapiens"
Db	202684	GGGTGACACCTGTGGCCATAGTAATGTACCACGGTGGTCCGGTGACACAGATGCAG	202743	gene	/db_xref="taxon:9606"
Qy	10441	CGCTGAGGGTTTTCTCAAGGTAAAGGAATGAAGATGGTGGAGGGCGTGCACTGGAA	10500	CDS	/map="6p"
Db	202744	CGCTGAGGGTTTTCTCAAGGTAAAGGAATGAAGATGGTGGAGGGCGTGCACTGGAA	202803		/chromosome="6"
Qy	10501	ATCAGTTGTAGAGAAAGCCCTGAAAAATTTGAGAAACAAACAAAGAACTACTTTACCAG	10560		/clone_lib="ICRF YAC-library"
Db	202804	ATCAGTTGTAGAGAAAGCCCTGAAAAATTTGAGAAACAAACAAAGAACTACTTTACCAG	202863		1028. 1324
Qy	10561	CTATTTGAATTTCTGGAATCACAGGCCATTGCTGAGCTGCCTGAAGTGGGAACACACAG	10620	intron	/gene="HFE"
Db	202864	CTATTTGAATTTCTGGAATCACAGGCCATTGCTGAGCTGCCTGAAGTGGGAACACACAG	202923	repeat_unit	1028. 10637
Qy	10621	AAGGAAACAAACCACTCTGATATCATTTGAGTCAAGTACAGCAGGTGATTGAGGACTGC	10680	repeat_unit	/gene="HFE"
Db	202924	AAGGAAACAAACCACTCTGATATCATTTGAGTCAAGTACAGCAGGTGATTGAGGACTGC	202983		join(1249. .1324,4652. .4915,5125. .5400,6494. .6769,
Qy	10681	TGAGAGTACAGGCCAAAATCTTATGTTGATATATAATGTCATCTTATAACTCTGT	10740	exon	6928. 7041,7995. .8035)
Db	202984	TGAGAGTACAGGCCAAAATCTTATGTTGATATATAATGTCATCTTATAACTCTGT	203043	intron	/gene="HFE"
Qy	10741	CAGTATTTATAAACAATCTTCCACAAACTCACACACATTTAAAAACAAACACACTGCTC	10800	exon	/function="iron metabolism"
Db	203044	CAGTATTTATAAACAATCTTCCACAAACTCACACACATTTAAAAACAAACACACTGCTC	203103	intron	/note="haemochromatosis candidate gene"
Qy	10801	TAAATCCCCAAATTTTTCATAAAC	10825	repeat_unit	/codon_start=1
Db	203104	TAAATCCCCAAATTTTTCATAAAC	203128	exon	/protein_id="CAB07442.1"
RESULT	12				/db_xref="GI:1890180"
LOCUS	HSHE				/translation="MGPRARPALLLLMLLTAVLQGLLRSLHVLPMGASRQDLGL
DEFINITION	Homo sapiens HFE gene.				SLEALGVDDQLFVFDHESRRVPEPTWSSRISSQMMQLQSILKGDMHFTVDF
ACCESSION	292910				WTIMENHNSKSHSTLQVILGCEQEDNSTPGEYKGYGDQDHLDFCPDTLDWRAEP
VERSION	292910.1				RAVPTKLEWRHKIRARONRAYLERDCPAQLQLLELGRVLDQVPLVKKVTHVTS
KEYWORDS	haemochromatosis; HFE gene.				SVTTLCRALNYYQNITMKWLKQPMDAKEFPKDLVLPNGDGTQGGTTLAVPPGE

QY	3897	GAAC	TCATGGGTTTCCAGT	AGAA	TTTCA	GCCAGATG	TGGCTGC	AGCTGAG	TCAGAGTC	3955
DB	4787	GAAC	TCATGGGTTTCCAGT	AGAA	TTTCA	GCCAGATG	TGGCTGC	AGCTGAG	TCAGAGTC	4846
QY	3957	TGAA	AGGTTGGGATCATG	TGTTCA	CTGTTG	ACTCTG	CTGAC	TATTTAT	TGGAAAA	4016
DB	4847	TGAA	AGGTTGGGATCATG	TGTTCA	CTGTTG	ACTCTG	CTGAC	TATTTAT	TGGAAAA	4906
QY	4017	ACAG	CAAGGTTATG	TGAG	CAGGGGG	CCCTCAC	CTTCTG	GAGTTGT	TCAGAGCT	4076
DB	4907	ACAG	CAAGGTTATG	TGAG	CAGGGGG	CCCTCAC	CTTCTG	GAGTTGT	TCAGAGCT	4966
QY	4077	TTTC	ATGCACTCTTGA	AGGAAAC	CAGCTG	GGAAGT	CTCTG	AGCTCTT	TGGGAGCAG	4136
DB	4967	TTTC	ATGCACTCTTGA	AGGAAAC	CAGCTG	GGAAGT	CTCTG	AGCTCTT	TGGGAGCAG	5026
QY	4137	GAAG	GAATTTGCTTCT	GAGATCA	TTTGGT	CTTGGG	GATGGT	GGAAT	TAGGACCT	4196
DB	5027	GAAG	GAATTTGCTTCT	GAGATCA	TTTGGT	CTTGGG	GATGGT	GGAAT	TAGGACCT	5086
QY	4197	CTTT	TGTTGCAGTTAAC	AAAGCTGG	GAATTTT	CCAGAGT	CCACAC	CCCTG	CAGAGTCAT	4256
DB	5087	CTTT	TGTTGCAGTTAAC	AAAGCTGG	GAATTTT	CCAGAGT	CCACAC	CCCTG	CAGAGTCAT	5146
QY	4257	CTT	GGGCTGTGAATC	GAAGAC	AACAGT	ACCGAG	GGCTACT	TGGAGT	TACGGGTAT	4316
DB	5147	CTT	GGGCTGTGAATC	GAAGAC	AACAGT	ACCGAG	GGCTACT	TGGAGT	TACGGGTAT	5206
QY	4317	TGGC	CAGGACCACTT	TGAATCTG	CCCTGAC	ACACTG	GGAAT	TGGAGC	ACGCAACCCAG	4376
DB	5207	TGGC	CAGGACCACTT	TGAATCTG	CCCTGAC	ACACTG	GGAAT	TGGAGC	ACGCAACCCAG	5266
QY	4377	GGCT	TGCCCCACCA	AGCTG	AGTGG	AAAGGC	ACAAGAT	TCGGCC	AGGCGAGACAGGC	4436
DB	5267	GGCT	TGCCCCACCA	AGCTG	AGTGG	AAAGGC	ACAAGAT	TCGGCC	AGGCGAGACAGGC	5326
QY	4437	CTAC	TGGAGAGGACTG	CCCTGC	ACAGT	GCAGC	AGTTG	TGGAGT	CGGGAGAGTGT	4496
DB	5327	CTAC	TGGAGAGGACTG	CCCTGC	ACAGT	GCAGC	AGTTG	TGGAGT	CGGGAGAGTGT	5386
QY	4497	TTTG	GACCAACAAG	TATGGT	GAAACAC	ACTTGC	CCCCAT	ACTCT	TAGTGGCAGAGTG	4556
DB	5387	TTTG	GACCAACAAG	TATGGT	GAAACAC	ACTTGC	CCCCAT	ACTCT	TAGTGGCAGAGTG	5446
QY	4557	GAG	AGGTTGCAGG	CACGGA	TCCTG	TGGAGT	TTTCAG	AGGTGGC	TGAGGCTGTGTG	4616
DB	5447	GAG	AGGTTGCAGG	CACGGA	TCCTG	TGGAGT	TTTCAG	AGGTGGC	TGAGGCTGTGTG	5506
QY	4617	CTCT	CCAAATCTCG	GAAAGG	ACTTTC	CAATCCT	ACAGTCT	CTAC	CTATATATTCAGA	4676
DB	5507	CTCT	CCAAATCTCG	GAAAGG	ACTTTC	CAATCCT	ACAGTCT	CTAC	CTATATATTCAGA	5566
QY	4677	TGT	ATGAGACGCC	ACAAGT	CAATG	GGTTTAA	TTTCTTT	CTCCAT	GCATATGGCTCAAG	4736
DB	5567	TGT	ATGAGACGCC	ACAAGT	CAATG	GGTTTAA	TTTCTTT	CTCCAT	GCATATGGCTCAAG	5626
QY	4737	GGA	GTGCTATG	CGCCCTTG	CTTTTAT	TTAACCA	ATAATCT	TGTATAT	TATATACCTG	4796
DB	5627	GGA	GTGCTATG	CGCCCTTG	CTTTTAT	TTAACCA	ATAATCT	TGTATAT	TATATACCTG	5686
QY	4797	TTAA	AAATTCAGAA	ATGTCA	AGCGGG	CACGGT	GGCTCAC	CCCCCTGT	TAATCCCAGCACTT	4856
DB	5687	TTAA	AAATTCAGAA	ATGTCA	AGCGGG	CACGGT	GGCTCAC	CCCCCTGT	TAATCCCAGCACTT	5746
QY	4857	TGG	GAGCCGAG	CGGGTGGT	TCAC	AGGTC	AGGAGTT	TG	GACACAGCCTG	4916
DB	5747	TGG	GAGCCGAG	CGGGTGGT	TCAC	AGGTC	AGGAGTT	TG	GACACAGCCTG	5806
QY	4917	TGAA	ACCCGCTCTCT	TAAAAA	ATAACAAAA	ATTAG	TGGT	CACAGT	CATCGCACCTGTAGT	4976
DB	5807	TGAA	ACCCGCTCTCT	TAAAAA	ATAACAAAA	ATTAG	TGGT	CACAGT	CATCGCACCTGTAGT	5866

Qy	4977	CCACGCTAA	TTGGAAGGCTGAGCAGGACGACATCGCTGTGAACCTGGGAACGGAAGTTGCA	5036
Db	5867	CCACGCTAA	TTGGAAGGCTGAGCAGGACGACATCGCTGTGAACCTGGGAACGGAAGTTGCA	5926
Qy	5037	CTGAGCCAA	GATCGCGCCACTGCATCTCCAGCCCTAGCAGCAGAGTGAGACTTCAATCTTAA	5096
Db	5927	CTGAGCCAA	GATCGCGCCACTGCATCTCCAGCCCTAGCAGCAGAGTGAGACTTCAATCTTAA	5984
Qy	5097	AAAAA	AAAAAAGAGAAATTCAGAGATCTCAGCTATCATATGAAATACCAAGGA	5156
Db	5985	AAAAA	AAAAAAGAGAAATTCAGAGATCTCAGCTATCATATGAAATACCAAGGA	6044
Qy	5157	CAAAATAT	CAAGTGAGCCCACTTATCAGAGTAGAAGAAATCCTTTAGGTATAAAGCTTCTT	5216
Db	6045	CAAAATAT	CAAGTGAGCCCACTTATCAGAGTAGAAGAAATCCTTTAGGTATAAAGCTTCTT	6104
Qy	5217	TCATAGAAC	ATAGCAATAATCACTAGAGCTACCTATCTTTACAAGTCCGCTTCTTATAACA	5276
Db	6105	TCATAGAAC	ATAGCAATAATCACTAGAGCTACCTATCTTTACAAGTCCGCTTCTTATAACA	6164
Qy	5277	ATGCCTCT	AGGTTGACCCAGGTGAACTTGACATCTGTATTCATCATTTTCAATGCAC	5336
Db	6165	ATGCCTCT	AGGTTGACCCAGGTGAACTTGACATCTGTATTCATCATTTTCAATGCAC	6224
Qy	5337	ATAAGGGCA	AAATTTTATCTATCAGAACAAAGAACATGGGTAAACAGATATGTATATTACA	5396
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COMMENT	Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerequest@sanger.ac.uk On Aug 27, 2000 this sequence version replaced gi:9864230. ----- Genome Center Center: Sanger Centre Center code: SC Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk ----- Project Information Center project name: BA557F22 ----- Summary Statistics Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 183925 bases at least Q40 Consensus quality: 187703 bases at least Q30 Consensus quality: 189658 bases at least Q20 Insert size: 192052; sum-of-contigs Insert size: 198247; agarose-fp Quality coverage: 3.68x in Q20 bases; sum-of-contigs Quality coverage: 3.70x in Q20 bases; agarose-fp ----- * NOTE: This is a 'working draft' sequence. It currently * consists of 18 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will		

* be preserved.			
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LOCUS
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Human hereditary haemochromatosis region, histone 2A-like protein
gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and
sodium phosphate transporter (NPT3) gene, complete cds.
ACCESSION
U91328
VERSION
U91328.1 GI:2088550
KEYWORDS
human.
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 246282)
AUTHORS
Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L.,
Domingo,R. Jr., Meyer,N.C., Irrinki,A., McClelland,E.E., Fullan,A.,
Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C.,
Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N.
A 1.1-Mb transcript map of the hereditary hemochromatosis locus
Genome Res. 7 (5), 441-456 (1997)
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MEDLINE
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REFERENCE
2 (bases 1 to 246282)
AUTHORS
Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L.,
Domingo,R. Jr., Meyer,N.C., Irrinki,A., McClelland,E., Fullan,A.,
Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C.,
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Direct Submission
Submitted (26-FEB-1997) Sequencing, Mercator Genetics, 4040
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QY	6421	TCTCAGAACCCAAATCTCGGTAGGGAATGAAATTTGATAGCAAGTAAATGCTAGTTAAAGAG	6480
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QY	6541	ATCACATTCACTGGGGATCAAGATAGCCTTCTGATCTTTGAAGGAGAGCTGGATTCCCA	6600
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DB	46959	GTGAATGAGGAAAATTAAGAGAGAGAGAGAGGCAAGATGGTGCCTTAGTGTCTGATGCGCT	46900
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DB	46899	CTTTTCTCGGCTCTGTGTCTCCACAGGAGGAGCCATGGGGCACTACGTCCTTAGCTGAAACG	46840
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Qy 10801 TAAATCCCAAAATTTTTCATAAAC 10825
Db 43179 TAAATCCCAAAATTTTTCATAAAC 43155

RESULT 15
AL353759
LOCUS
DEFINITION

AL353759 101099 bp DNA linear PRI 05-SEP-2001
Human DNA sequence from clone RPI-221C16 on chromosome 6. Contains the 3' part of the HFE gene for haemochromatosis protein, two genes for novel histone 4 family members, two genes for novel histone 1 family members, three genes for novel histone 2B family members, a gene for a novel histone 2A family member, a novel pseudogene, STSS, GSSs, ESTs and CpG islands, complete sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL353759.8 GI:8745068
HTG: CpG island; H1; H2A; H2B; H4; haemochromatosis; HFE; histone. human.

REFERENCE
AUTHORS
TITLE
JOURNAL

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101099)
Williams, S.
Direct Submission
Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT

On Jun 26, 2000 this sequence version replaced gi:8655345.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPI-221C16 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: PCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RPI-221C16 it may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RPI-221C16 is at 1 in this sequence. The true left end of clone RPI-34B20 is at 101000 in this sequence.

FEATURES
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mRNA


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3176
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and assembly confirmed by restriction digest."
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4816..4979
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5232..5532
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5547..5825
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6160..6457
/ note="AluSg repeat: matches 1..299 of consensus"
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6888..7194
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8017..8062
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Tr:Q9QVB5 Sw:P06350 Sw:P15865 Tr:Q91369 Sw:P16402
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SKK"
15369..15581
/ note="AluJo repeat: matches 1..261 of consensus"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GATCTTGAAGGAGAAGCTGGATTCATTAGGTGAGGTTGAAGATGATGGAGGCTACAC 60
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Qy 8735 TCCTCTGTGTCTCTTTGGCATTTCTTTGGACCTTACGCAAGGACTGTAATTTGGT 8794
Db 2161 TCCTCTGTGTCTCTTTGGCATTTCTTTGGACCTTACGCAAGGACTGTAATTTGGT 2220
Qy 8795 GGGGACAGCTAGTGGCCCTGCTGGGCTTACACACAGGTGTCTCCCTAGGCCAGTGCCCTC 8854
Db 2221 GGGGACAGCTAGTGGCCCTGCTGGGCTTACACACAGGTGTCTCCCTAGGCCAGTGCCCTC 2280

QY	8855	TGGAGT	CAGAACTCTGGTGGTATTTCCCTCAATGAAGTGGAGTAAAGCTCTCTCAFTTTGA	8914
Db	2281	TGGAGT	CAGAACTCTGGTGGTATTTCCCTCAATGAAGTGGAGTAAAGCTCTCTCAFTTTGA	2340
QY	8915	GATGTA	TAAATGGAAGCACCAAGTGGCTTAGAGGATGCCAGGTCCTTCCATGGAGCA	8974
Db	2341	GATGTA	TAAATGGAAGCACCAAGTGGCTTAGAGGATGCCAGGTCCTTCCATGGAGCA	2400
QY	8975	CTGGGGT	CCGGTGCACATTAATAAAAAAATCTAAACAGGACATTCAGGAATTCGTAGAT	9034
Db	2401	CTGGGGT	CCGGTGCACATTAATAAAAAAATCTAAACAGGACATTCAGGAATTCGTAGAT	2460
QY	9035	TCTGGAAAT	CAGTTCACCATGTTCAAAGAGTCCTTTTTTTTTTTTTTTTTTTTGAGACTCTATTG	9094
Db	2461	TCTGGAAAT	CAGTTCACCATGTTCAAAGAGTCCTTTTTTTTTTTTTTTTTTTTGAGACTCTATTG	2520
QY	9095	CCAGGCT	GGAGTGCATGATCTCGGCTCACTGTAACCTCTGCCTCCAGGATTC	9154
Db	2521	CCAGGCT	GGAGTGCATGATCTCGGCTCACTGTAACCTCTGCCTCCAGGATTC	2580
QY	9155	AGCATTCT	CTCGTCTCAGCCTCCCAAGTAGCTGGGATACAGGCGTGCACACCATGCC	9214
Db	2591	AGCATTCT	CTCGTCTCAGCCTCCCAAGTAGCTGGGATACAGGCGTGCACACCATGCC	2640
QY	9215	CGGCTAAT	TTTTTGTATTTTTTAGTAGACAGAGGTTTTACCATGTTGGCCAGGCTGGTCTC	9274
Db	2641	CGGCTAAT	TTTTTGTATTTTTTAGTAGACAGAGGTTTTACCATGTTGGCCAGGCTGGTCTC	2700
QY	9275	GAACCTCT	CCGTGACCTCGTGATCGCCTCGCTCGGCTCCCAAGTGCTGAGATTACAGGT	9334
Db	2701	GAACCTCT	CCGTGACCTCGTGATCGCCTCGCTCGGCTCCCAAGTGCTGAGATTACAGGT	2760
QY	9335	GTGAGCC	CCCTGCCAGCCGTCAAAAGAGTCTTAATATATATATCCAGATGGCATGTGT	9394
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QY	9455	AGGCAGG	CTGCTCAGGATACCATATACAGCTCAGAAGTTCTTCTTTTAGGCAATTAATTT	9514
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QY	9755	GCATGATTT	TATTGAAAGTTCTTTGTCATCTTGATATATCTTAATCGCTTTGTCATTTT	9814
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QY	9815	GGAGACAT	TATTTCGTTCTAATTTCTTTACATTTTGCTCTTAGGAAATATTTCATCA	9874
Db	3241	GGAGACAT	TATTTCGTTCTAATTTCTTTACATTTTGCTCTTAGGAAATATTTCATCA	3300
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Db	3301	ACTGTGGT	AGCCGAATTAATCGTGTCTTCTCACTCTAGGACATTCGCTCAAGTTGTA	3360
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QY	10235	TTTCTTCGGTGTTTTTAAAGCTTAATTTTCTGGCTTTATTTCAATAATCTTAAAGTCA	10294
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QY	10415	CGGTGGTCCGGTACCGAGATGCAGCCTGAGGGTTTTCTGAGGTAAAGGAATAAG	10474
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Db	4081	AAGTACAGCAGGTGATTTGAGGACTGCTGAGAGGTACAGGCCAAAATTTCTTATGTTGTATT	4140
QY	10715	ATAATATGTCATCTTATAATCTCTCAGTATTTTATAAACATTTCTTCAAACTCACA	10774
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QY	10775	CACATTTAAACAAAAACACTGTCTTAAATCCCAAAATTTTTCATAAAC	10825
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Search completed: June 19, 2002, 22:41:45
Job time: 29342 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 14:28:33 ; Search time 993.62 Seconds
(without alignments)
18704.936 Million cell updates/sec

Title: US-09-497-957-1

Perfect score: 10825
Sequence: 1 TCFAAGGTGAGATAAAATT.....TCCCAAAATTTTCATAAAC 10825

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

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- 23: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10823	100.0	10825	22 AAC68425	Human hereditary h
2	10823	100.0	10825	22 AAC68426	Human hereditary h
3	10823	100.0	10825	22 AAC68427	Human hereditary h
4	10823	100.0	10825	22 AAC68428	Human hereditary h
5	10816.6	99.9	10825	18 AAT96690	Hereditary haemoch
6	10759.8	99.4	12146	21 AAA96794	Genomic DNA of a h
c 7	10707	98.9	237326	19 AAV57903	Hereditary haemoch
c 8	5724.8	52.9	5749	22 AAL36747	Human musculoskele
c 9	3109	28.7	235033	19 AAV57926	Hereditary haemoch

c 10	2556.4	23.6	8622	24 ABL34142	Human immune syste
c 11	2248.8	20.8	8622	24 ABL34143	Human immune syste
c 12	1712	15.8	1712	22 AAL36748	Human musculoskele
c 13	1051.6	9.7	2506	21 AAA96769	CDNA sequence enco
c 14	1051.6	9.7	2727	19 AAV23525	Haemochromatosis g
c 15	516	4.8	517	22 AAC68440	Human hereditary h
c 16	516	4.8	517	22 AAC68441	Human hereditary h
c 17	493	4.0	1110	22 AAL36752	Human musculoskele
c 18	395.2	3.7	12127	22 ABA08204	Human ovarian and
c 19	395.2	3.7	12127	22 AAL07512	Human reproductive
c 20	395.2	3.7	12127	22 AAS28679	Genomic sequence #
c 21	384	3.5	384	22 AAL36751	Human musculoskele
c 22	358	3.3	359	20 AAX16055	Hereditary hemochr
c 23	357.6	3.3	161425	22 AAH02340	Human AKAP10 gene
c 24	357.6	3.3	162025	22 AAH02339	Human AKAP10 gene
c 25	355.8	3.3	14796	19 AAV27941	Survivin gene. Ho
c 26	355.8	3.3	14796	22 AAS21523	DNA encoding human
c 27	355.8	3.3	14796	22 AHA47531	Human Her-3 genomi
c 28	355	3.3	48045	22 AAK84730	Human immune/haema
c 29	355	3.3	48045	22 AAK85984	Human immune/haema
c 30	351.2	3.2	32190	22 AAS36709	Human cardiovascular
c 31	347.8	3.2	48037	22 AAK84729	Human immune/haema
c 32	347.8	3.2	48037	22 AAK85983	Human immune/haema
c 33	344	3.2	12169	22 AAK81443	Human immune/haema
c 34	344	3.2	12164	22 AAK79678	Human immune/haema
c 35	338.6	3.1	14781	22 AAL36303	Human musculoskele
c 36	337.6	3.1	31885	22 ABA19143	Human nervous syst
c 37	337.6	3.1	31885	22 AAL36165	Human musculoskele
c 38	337.6	3.1	31885	22 AAL36176	Human musculoskele
c 39	337.6	3.1	31885	22 AAL04523	Human reproductive
c 40	337.6	3.1	31885	22 AAS28341	Genomic sequence #
c 41	337.6	3.1	52845	22 AAK71437	Human immune/haema
c 42	337.2	3.1	32763	22 AAK68779	Human immune/haema
c 43	336.6	3.1	32187	22 AAS32249	Human DNA repair a
c 44	336.4	3.1	12473	22 ABA18817	Human nervous syst
c 45	334.2	3.1	53552	22 AAS13655	Genomic DNA sequen

ALIGNMENTS

RESULT 1
AAC68425
ID AAC68425 standard; DNA; 10825 BP.
AC AAC68425;
XX
XX 21-FEB-2001 (first entry)
XX
XX Human hereditary hemochromatosis DNA.
XX
XX HH; hereditary hemochromatosis; chelation agent;
XX
XX T-cell differentiation factor; iron overload; ds.
XX
XX Homo sapiens.
XX
XX US6140305-A.
XX
XX 31-OCT-2000.
XX
XX 04-APR-1997; 97US-0834497.
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XX 04-APR-1996; 96US-0630912.
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XX 16-APR-1996; 96US-0632673.
XX
XX 23-MAY-1996; 96US-0652265.
XX
XX (BIRA) BIO-RAD LAB INC.
XX
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
XX
XX Feder JN;
XX
XX WPI: 2001-006341/01.
XX
XX P-PSDB; AAB36869.

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RESULT 2
AAC68426
ID AAC68426 standard; DNA; 10825 BP.
AC AAC68426;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d1 mutation DNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ds.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PE 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI: 2001-006341/01.
DR P-PSDB; AAB36870.

XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;

Query Match 100.0%; Score 10823; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 2161 aaactttgcacatgtcacttagtagaacaactcctcgtttaagaagctcgggttgaaaaa 2220
QY 2221 AATAAACAGTAGTGTCTGGGGAGTAGAGGCCAAAGATAGGTAATGGGCTCAGAGAGGA 2280

Db 2221 aataaacaagttagtgcgtg99gagtagagggccaagaagtagtaattg99gctcagaagagga 2280
QY 2281 GCCACAAACAAGGTTGTGACGGCGCCTGTAGGCTGTGGTGTGAATTTAGCCACGAGGTA 2340
Db 2281 gcccacaaacaagggttgtgcaggccctgtaggctgtggtgtgaattctagccaagagta 2340
QY 2341 ACAGTGATCTCTCACAGGCTTTTAAAAAGATTGCTCTGGCTGTATGTGGAAAGCAGAAATG 2400
Db 2341 acagtgatctgtcacaggcttttaaaagattgctcgtggtctatgtggaagcagaatg 2400
QY 2401 AAGGGAGCAACAGTAAAGCAGGGGAGCCACGACGAGGAGCTTTACACAGTCCAGGCAAG 2460
Db 2401 aaggagacaacagtaaaagcaggagccagccagcagggaagctgttcacacagtccagggcaag 2460
QY 2461 AGGTAGTGAGTGGGCTGGGTGGGAACAGAAAAGGGAGTGACAAACCATGTCTCTCTGAA 2520
Db 2461 agttagtgaggtg99gctgggtgggaacagaaaaggagtgacaaacctgtctcctgaa 2520
QY 2521 TATATTCTGAAGGAAGTTGCTGAGGATCTTATGTGTGTGAGAGAAAGACAGAAATTTG 2580
Db 2521 tataattctgaaggaaagttgctgaaggattctatgtgtgtgagagaaagagaatctgg 2580
QY 2581 CTGGGTGTAGTAGCTCATGCTCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA 2640
Db 2581 ctg99gtgtgtagtagctcatgccaaggagag99ccaaggagagcagatctctgagctcagga 2640
QY 2641 GTTCAAGCACCGCTGGGCACACAGCAAAACCCCTTCTCTACAAAATAATACAAAATTA 2700
Db 2641 gttcaagcacagcctgggcaacacagcaaaaccccttctacaaaaatacaaaaatta 2700
QY 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCTAGCTACTCGGGAGGCTGAGGTGGAGGTA 2760
Db 2701 gctg99gtg99g99catgcacctgtgtactactgtactcctcactcggag99gta 2760
QY 2761 TTGCTTTGACCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTTCAGC 2820
Db 2761 ttgctttgagcccaggaagttaggctgagctgagccatgtactgtgccactgtacttcagc 2820
QY 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTCACCCCTGAAAAAGAGAAGAGTTAAAGT 2880
Db 2821 ctagggtgacagagcagacccctgtcccccctgaccccctgaaaaagagaagagttaaagt 2880
QY 2881 TGACTTTGTCTTTATTTTAAATTTTATTTGGCCTGAGCAGTGGGGTAAATTTGGCAATGCCAT 2940
Db 2881 tgaactttgtctttatttaattttattgtgctgagcagtg99gtaattggcaatgccat 2940
QY 2941 TTCTGAGATGGTGAAGGCAGAGAAAGACAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000
Db 2941 ttctgagatgggtgaaggcagaggaagagcagtttggggtaaatcaagatctgcatctg 3000
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Db 3001 ggaca tgttaagtgtgagattccagtcaggcttcccaagtgtgag99gccaacatagcagctt 3060
QY 3061 CAGTGTAAAGAAATTCAGAGACCAAGGCTGGGACGGTGCACGTGCTACTTCTGTAAATCCCAGCACT 3120
Db 3061 cagtgtagaataatcagagaccagcctg99cagcagtggtcactctctgttaatccccagcact 3120
QY 3121 TTGGTGGCTGAGGCAGGTAGATCATTTTGAGTCCAGAGTTTGAGACAAAGCTTTGGCCCAACA 3180
Db 3121 ttggtggctgaggcaggtagatcatttgaggtcagaggtttgagacaagcttggcccaaca 3180
QY 3181 TGGTGAACCCCATGTCTACTAAAAATACAAAATTTAGCCTGTGTGGTGGCGCACGCCCT 3240
Db 3181 tgggtgaaccccatgtctactataaaaatacaaaaaattagcctggtgtg99g99cagcagcct 3240
QY 3241 ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAAATFCCCTTGAACCCAGGAGGTGCAGG 3300
Db 3241 atagtcccaggttttccagggagcttaggttaggagaa tcccttgaaacccagggaggtcag 3300
QY 3301 TTGCAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGTGATAGAGTGACACTCTGT 3360
Db 3301 ttgcagtgcagctgagattgtgcactgcactccagcctgg99gtgatagagtgagactctgt 3360

QY	3361	CTCAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAAATTATTCCTCAGGATTTGGG	3420
Db	3361	ctcaaaaaaaaaaaaaaaaaaaaaaaactgaaggaatttattcctcaggatttggg	3420
QY	3421	TCTAATTGGCCTGACGCCAACTCCTGAGTTCACACTACCATTGGCTAGACACACCTTAAC	3480
Db	3421	tctaattggccctgagaccaaacctcctggtccaactaccatggctagacacacctLaac	3480
QY	3481	ATTTTCTAGAATCACACAGCTTAGTGAGTCTGTCTAATCATGAGTATTGGAATAGGAT	3540
Db	3481	attttctagaatccacagccttagtggaagtctgtctaatcatdagtatggaaataggat	3540
QY	3541	CTGGGGCGATGAGGGGGTGGCAGCCACGTGGCAGAGAAAACACACAAGAGAAAGGC	3600
Db	3541	ctggggcgatggagggggtggcagccaogtfggcagagaaaagcacacaaggaagagc	3600
QY	3601	ACCCAGGACTCATATGGAAGAAAGACAGGACTCCAACCTCACCTTTCACAAATGAGGA	3660
Db	3601	accaggactctatatggagaagaagacaggctgcacactcaccttcacaaataggga	3660
QY	3661	CCAGACACAGCTGATGGTATGATGTGATSCAGSGTGTGGAGCCTCAACATPCTGCTCCC	3720
Db	3661	ccagacacagctgatggtatgattgatgcaggtgtgfgagcctcaacatcctgctccc	3720
QY	3721	CTCCTACTACACATGTTAAGGCCCTGTGCTGTCTCTCCAGGTTCAACACTCTCTGCACTA	3780
Db	3721	ctcctactacacatggttaaggccctgtgtctgtctctccaggttcacactctctgacta	3780
QY	3781	CCTCTCATGGGTGCCCTCAGACAGGACOTTGGTCTTTCCTTGTGAAGCTTTGGGCTA	3840
Db	3781	cctctcatgggtgccctcagacaggacotlggtcttctcttcttggtgaagctttgggcta	3840
QY	3841	CGTGGATGACCACTGTTTCGTGTTCTATGAINATCAGAGTCCGCGTGTGGAGCCCCGAAC	3900
Db	3841	cgf9gatgaccagctgttcgtttctatafgactagagatgcgcgtgtggagccccgaac	3900
QY	3901	TCCATGGGTTTCAGTAFGAATTTCAAAGCCAGATGTGGCTGCAGCTGAGTTCAGAGTCTGAA	3960
Db	3901	tccatgggtttccagttagaattccaagccagatgtggctgcagctgagtcagagctgtaa	3960
QY	3961	AGGTTGGGATCACATGTTTCACTGTTGACTTCTGGACTATTATGAAAATACAAACACAG	4020
Db	3961	agg9ttgggatacaatgttcaactggttgactgtgactattatggaaaatcaccaaccag	4020
QY	4021	CAAGGTTATGTGAGAGGGGGCCTCACCTTCTGAGGTTGTACAGCTTTTTCATCTTTTC	4080
Db	4021	caa9gtatgtggagaggggacctcaecttctgaggltgccagagcttttcatcttttc	4080
QY	4081	ATGCATCTTGAAGGAACAGCTTGAAGTCTGTGAGTCTTGTGGGAGCAGGGAAGGGAAG	4140
Db	4081	atgcatcttgaaggaaacagctggaagtctgaggtcttggtggagcagggaagaggaag	4140
QY	4141	GAAATTGCTTCCTGAGATCATTTTGCTCTGGGATGTGGAAATAGGACCTATTTCCTT	4200
Db	4141	gaatttgcttctgagatcaatttggccctgg9gat9gt9gaatatgg9accatctcctt	4200
QY	4201	TGTTTGCAGTTAACRAGGCTGGGATTTTTCCAGAGTCCACACCCCTGCAGGTCATCCTG	4260
Db	4201	tgg9ttgcagttaacaaggctgg9gggttttccagagttcccaacctgcaggtctcctg	4260
QY	4261	GGCTGTGAATGCAAGAGACAACTAGTACCAGGGCTACTTGAAGTACGGGTATGATGGG	4320
Db	4261	ggctgtgaatatgcaagagacaacagtagtaccgaggggttac-tggaagtacgg9tatg9g9	4320
QY	4321	CAGGACCACTTTGAATCTTGCCCTGACACACTGGATTGGAGCAGCAGAACCCAGGGCC	4380
Db	4321	caggacaccttgaaattctgccctgacacactggtatggagcagcagaaccagg9cc	4380
QY	4381	TGSCCCCAACACTGGAGTGGGAAGGCACAAGATTTCGGGCCAGGCAGAACAGGGCCTAC	4440
Db	4381	tggccccaacagctggagtg9gaaaggcaagatctgg9ccagggagacaagggcctac	4440

QY	4441	CTGAGAGGGGACTGCCTCTGCACAGCTGCACAGCTGCCTGGAGCTGGCGAGAGGTGTTTG	4500
Db	4441	ctgagaggggactgcctctgcacagctgcacagctgcctggagctgggagaggtgttttg	4500
QY	4501	GACCAACAAGGTATGGTGGAAACACACACTCTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560
Db	4501	gaccaacaaggatggtgggaacacacactctgcctccatactctagtgccagatggagg	4560
QY	4561	AGGTTGCAGGCGCCGGAATCCCTGGTTTGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Db	4561	aggttgcaggcgccgaataccctgggttgagtttcagaggtggctgaggtgtgtgcctc	4620
QY	4621	TCCAAATCTCTGGGAAGGACCTTTCTCAATCCCTAGAGTCTCTACCTTATAATTGAGATGTA	4680
Db	4621	tccaaattcttgggaagggaacttctcaaacctagtagtctctaccctcaaatgtgagatgta	4680
QY	4681	TGAGACAGCCACAGTCATGGGTTTAATTCTTTCTTCATGCATATGGCTCAAAAGGAA	4740
Db	4681	tgagacagccacaagtcattgggtttaatttcttccatgcatactgtcctcaaggaa	4740
QY	4741	GTGCTATGGCCCTGCTTTTATTTAAACCAATATCTTTGTATATTATACCTGTAA	4800
Db	4741	gtgctatggccctgccttttatttaacccaataacttcttgatatattatcacctgttaa	4800
QY	4801	AAATTCAGAAATCTCAAGCGCGGACGGTGCTCACCCCTGTATCCCGACACTTTGGG	4860
Db	4801	aaattcagaatgtcaaggcgcggaacgtgctcaacctgttaatcccgacctttggg	4860
QY	4861	AGGCCGAGCGGGTGTCTACAAGTCAGAGTTTGAGACGACGCTGACCACATGTTGAA	4920
Db	4861	aggccgaggcggttggttcaaaagttcaggagtttgagaccagctgaccaacatggtaa	4920
QY	4921	ACCCGCTCTTAAAAAATAACAAAATTAGCTGGTCACAGTCATGCGACACTGTAGTCCCA	4980
Db	4921	accgctcttataaaaaatacaaaaattagctggttcacagtcacgtgcactgtagtcoca	4980
QY	4981	GCTAATTGGAAGGCTCAGGCGAGGACATCGCTTGAACTCTGGGAGCGGAAGTTGCACATGA	5040
Db	4981	gctaattgggaagctgaggcaggagcactcgcttgacctgggaagcggaagtgtcactga	5040
QY	5041	GCCAAGATCGCGCACTGCACACTCCAGCCTTAGCGACGACAGTGAGACTCCATCTTAAAAA	5100
Db	5041	gccaaagtgcgccaactgcactccagctaggcagcagagtgagactccattcaaaaa	5100
QY	5101	AAAAAATAAATAAAGAGAAATTCAGAGATCTCAGCTATCATATGAATACCGAGACAA	5160
Db	5101	aaaaaataaataaagagaattcagagatcctcagctcagctatcatatgaataccaggacaaa	5160
QY	5161	ATATCAAGTCAGCGCACTTATCAGAGTAGAAGAACCTTTTAGGTTAAAGTTTCTTTCAT	5220
Db	5161	atatcaagtgaggccactatcagagtagaagaatcccttaggttaaaggtctcttcat	5220
QY	5221	AGAACATAGCAATTAATCACTGAAGCTACTCTTCTACAAGTCCGCTCTTTATACCAATGC	5280
Db	5221	agaacatagcaataatcaactgaagctacctattctacaagtcgcgtctctataacaatgc	5280
QY	5281	CTCCTAGGTTGACCGAGGTGAACCTGCACATCTGATTTCATATTTTCAATGTCACATAA	5340
Db	5281	ctcctaggttgacccaggtgaactgacactgctgtattcaatcatcttcaatgacataa	5340
QY	5341	AGGCAATTTTATCTATCAGAAACAAGAACATGGGTAAACAGATATGATATTACATGTG	5400
Db	5341	aggcaattttatctatcagaacaaagaacatgggttaacagatgcatattcacatgtg	5400
QY	5401	AGGAGAACAGCTGATCTGACTGCTCTCCAAGTCACACTGTGTTTAGAGTCCCAATCTTAGG	5460
Db	5401	aggagacaagctgactgactgctctccaagtgaacactgtgttagagtcaccaatcttagg	5460
QY	5461	ACACAAAATGGTCTCTCCTAGCTTGTGTTTTTCTGTAAAAGGGTATTTCTTCTCTCC	5520
Db	5461	acacaaaatgggtctctcctagcttgtgtttttctgtaaaagggtatttctctctccc	5520
QY	5521	AACTATAGAAGGAGTGAAGGTTCCAGTCTCTCTGCGCAAGGGTAAACAGATCCCTCTC	5580

Qy	7741	GCACCTGTCCCGAGAAAAAGCATCATGGCTATCTCTGGGTAGTATGATGGGTGTTTTAGC	7800
Db	7741	gcacctgtcccagaaaaagcatcatggctatctctgggtagtatgatgggtgtttttagc	7800
Qy	7801	AGGTAGGAGGCAAAATATCTTGAAAGGGGTGTGGAAGAGGTGTTTTTCTAAATFGGCATGA	7860
Db	7801	aggtaggaggcaaatatcttgaaggggttgtgaagagggtgttttcttaattggcgatga	7860
Qy	7861	AGGTGTATACAGATTGCCAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT	7920
Db	7861	aggtgtatcacagatttgcaagtttaatgggtgccttcaattg99gaugtcactcctagtat	7920
Qy	7921	TCCAGACCTTGAAGAATACAATAATTTCTACCTGGTCTCTCCCTGTGTTGATAATGAAA	7980
Db	7921	tccagacctgaagaatcacataattttctacotggctctcctctgtctctgataatgaaa	7980
Qy	7981	ATTATGATTAAGATGATTAAGAAGCACTPACTTCGTGTCGGACTCTCTTGAGCACCCTACTTA	8040
Db	7981	attatgataaggatgataaagcacttactctgtctgcagactctcttgagcacttactta	8040
Qy	8041	CATGCATTACTGCATGCACCTCTTCAACAATAATCTATGAGATAGGTACTATTATCCCCAT	8100
Db	8041	catgcattactgcatagcactctcttaacaataattctatgagataggtactattatcccat	8100
Qy	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTAGGGCGGCACGGTGGCTCACGCCCTGTAAATCCC	8160
Db	8101	ttcttttttaaatgaagaaagtgaagtagggcgggcgacgggtggctcacgctgtaatccc	8160
Qy	8161	AGCACTTTGGGAGGCCAAAGCGGGTGGATCAGGAGGTGAGAGATCAGACCACTCCTGGC	8220
Db	8161	agcaccttgggaggccaaagcggtggatcacagaggtcaggagagatcgagaccactctggc	8220
Qy	8221	TAACATGGTGAACCCCACTCTCTAATAAAATACAAAAATTAAGTGGGGTGGTGGCAG	8280
Db	8221	taacatggfgaaaccccatctctaataaaatacaaaaaattagctgggcgtggtggcag	8280
Qy	8281	ACGCCGTGTAGTCCAGCTACTCGGAAGGCTGAGGCAGGAGATGGCATGAACCCAGGAGG	8340
Db	8281	acgccgtgtgtccagctactcggaggctgagcgaggagaatggcatgaaccagagg	8340
Qy	8341	CAGAGCTTGCAGTAGGCCAGTTGGCCACTGTGCACTCCAGCCTAGGTGACAGAGTGAGA	8400
Db	8341	cagagcttgcagtgagccgaggttgcgcactgcactccagccttaggtgcagagtgaga	8400
Qy	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATGAAAAAAGAAAAAGTGAAGTA	8460
Db	8401	ctccatctcaaaaaataaaaaataaaaaatgaaaaaaagaaagtgaagta	8460
Qy	8461	TAGAGTATCTCATAGTTTGTCAGTGATGAACAGAGTTTCAAACTCAGTCAATCTGACCG	8520
Db	8461	tagagtatctcatagtttgcagtgatagaacaggtttcaaacctcagtcactctgaccg	8520
Qy	8521	TTTGATACATCTCAGACACCACTACATTCAGTAGTGTTAGTCCCTAGATAAATAGAGAA	8580
Db	8521	tttgatacatctcagacaccactacattcagtagtttagatgcctagataaataagagaa	8580
Qy	8581	GGAAGGAGTGGGTCTTCTTGTGCTATGTTGTTCTTCTGTAGTGAGCTTGAATCATCAT	8640
Db	8581	ggaaggagatggctctctcttctgtctcatgtgttctctcgtgagcttgaatcatcat	8640
Qy	8641	GAAGGGAAACAGCAGAAAAACAACCAACTCATCTCAGCTGTCTATGTTTCCTTTAAAAAGTC	8700
Db	8641	gaaggggaaacagcagaaaaaaccaactgatctctcagctgtcatgttttccctttaaaagtc	8700
Qy	8701	CCTGAAGGAAGGTCCTGGAAATGTGACTCCCTCTCTCTCTGTGTGCTCTCTTTGGCATATCA	8760
Db	8701	cctgaaggagggtccctggaaatgtgactccctctctctctgtgtctctcttcttggcattca	8760
Qy	8761	TTTCTTTGGACCCCTACCCAGGACTGTAAATTTGGTGGGACACAGCTAGTGGCCCTGCTGGGC	8820
Db	8761	tttctttggacctacgcaagagactgtaattggtgggacagcagtagtgccctctgggc	8820

Qy	8821	TTCACACAGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTCGTGGTATTTC	8880
Db	8821		8880
Qy	8881	CTCTCAATGAAGTGGCATGAAGCTCTCTCATTTTGGAGATGGTATATATGAAGCCACCAAGTg	8940
Db	8881		8940
Qy	8881	CTCTCAATGAAGTGGCATGAAGCTCTCTCATTTTGGAGATGGTATATATGAAGCCACCAAGTg	8940
Db	8881		8940
Qy	8941	GCTTAGAGGATGCCAGGCTCTTCCATGGAGCCACTGGGGTTCGGGTGCACATTAATAAAA	9000
Db	8941	gcttagaggaTgcccaggTccctccatggagccactgggttccoggtgcacattaaaaa	9000
Qy	9001	AAAATCTAACCGAGGACATTCAGSAATGCTAGATTCTCGGAAATCAGTTCACCATGTTCA	9060
Db	9001	aaaatctaaacggagacatTcaggaaTctgtagatTctgggaaTcagTtccacatgtcca	9060
Qy	9061	AAAGAGTCTTTTTTTTTTTTTTTGAGACTCTATTGCCAGGCTGGAGTGCAAATGGCATGAT	9120
Db	9061	aaagagTcttt	9120
Qy	9121	CTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCCATTCCTGTCTCAGCGTCCCA	9180
Db	9121	ctcggtccactgTaaactctgctccaggTtcaaagcatTctcctgtctcagctcccca	9180
Qy	9181	AGTAGCTGGGATTACAGGGGCTGCACACCATGCCGGGCTAAATTTTGTATTTTAGTAGA	9240
Db	9181	agtagctTgggaattacaggogTgcacacccatgcccgctaattttgtatttttagtaga	9240
Qy	9241	GACAGGTTTCACATGTTGGCCAGGCTGGTCTCGAACTCTCTGACCTCGTGATCGCC	9300
Db	9241	gacagggtttcaccatgttgccaggctggTctcgaaTctcctgacctgtgacgcgc	9300
Qy	9301	TGCCTCGGCTCCCAAGTCTCAGAGTTACAGGTGTGAGCCACCTGCCACCGCTCAAA	9360
Db	9301	TgcctcggcctcccaaggTctgagattacaggTgtgagccacctgcccagccgtcaaa	9360
Qy	9361	AGAGTCTTAAT	9420
Db	9361	agagTcttaatatataTatccagatggcatgtgttactttatgttactacatgcaactg	9420
Qy	9421	GCTGCATAAATGTGGTACAAGCATCTGTCTTAAGGGCAGGTGCTTCAGGATACCATAT	9480
Db	9421	gctgcataaaTgtggtcacagcattctgttgaaaggcaggtgcttcaggataccatat	9480
Qy	9481	ACAGCTCAGAAAGTTCTCTTTTAGCCATTAATTTTAGCAAAAGATATCTCATCTCTCT	9540
Db	9481	acagctcagaagTttcttcttttaggcattaaatttttagcaagaTatctcatctctctt	9540
Qy	9541	TTAAACCATTTCTTTTTTTTGGTTAGAAAGATTATAGAAAAAGATAAATGTGATTT	9600
Db	9541	TtaaaccatttcttttttttTgTgtagaaaagTatgTgaaaaaagTcaaatgTgattt	9600
Qy	9601	ACGCTCATTTGTAGAAAAGCTATAAATGAATACAAATTAAGCTGTTATTTAATTAGCCAG	9660
Db	9601	acgctcatTtagaaaagcTataaaatgaatacaaatTaaagctgttatttaatltagccag	9660
Qy	9661	TGAAAAACTATTACAACTGTCTATTACCTGTTAGTATTATTTGTCATTAATAATGCA	9720
Db	9661	TgaaaaactattTaaacaactgtctattacactgttagTattttgttgcatTaaaaatgca	9720
Qy	9721	TATACTTTTAATAATGTATATTGTATGTATCTGCATGATTTTATGAAGTCTCTGTTC	9780
Db	9721	TatactttTaaataatgtatattgtattgtatactgcatacttttatTgaagttctgttct	9780
Qy	9781	ATCTGCTGTATATACTTAATGCGTTCATATTTTCACTGTTGGAGACATTTATTTGCTCTAATTT	9840
Db	9781	atctTgtgtataTactttaactgcctgttgcattttttggagacattttatttgcctctaattt	9840
Qy	9841	CTTTACATTTTGTCTTACGGTAATTTTTCATTTCACTGTTGGAGCAATTAATTCGTGTT	9900
Db	9841	ctttTaatTTTgtctTcaTcggaattttTcattTcaactgtTggtagccgaattaatcgTctt	9900
Qy	9901	TCTTCACCTCTAGGGACATTTGCTGCTCAAGTGTGAAGACATTTGTTATTTTACCACCAAC	9960

Db 9901 tcttcaacttaaggacattgctgcttaagttgtaagacatggttatattaccagcaaac 9960
QY 9961 CATTTCTGAAGCATATGACAAATTAATTTCTCTCTTAATATATTACTATACATGAAAGCAGA 10020
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QY 10081 AGGTAAGCAATTTGTTTATTTATTTGTTTATTTTCACTGGGCTGAGATTTCAAGAAACACC 10140
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QY 10141 CCAGTCTTCACAGTAACACATTTCACTAACACATTTTACTAAACATCACCACTGTGCCT 10200
Db 10141 ccagcttccacagtaaacacatttcaataaacacatttactaaacatcagcaactgtgacct 10200
QY 10201 GTTAATTTTTTAATAGAAATTTAAGTCCTCATTTTCTTCGGTGTTTTAAAGCTTAA 10260
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QY 10261 TTTTCTGGCTTTTATCATAAATTTCTTAAGTCAACTACATTTGAAAAATCAAGACCTG 10320
Db 10261 tttttctggtttattcataaattcttaaggtaacatactatttgaaaataccaagacctg 10320
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QY 10741 CAGTATTTTAAACAAATTTCTCACAACTCACACATTTTAAAAACAAACACTGCTCTC 10800
Db 10741 cagtattttataaacattcttcacaaactcacacatttataaaacaaacaaactgtctc 10800
QY 10801 TAAATCCCCAAATTTTTCATAAAC 10825
Db 10801 taaaatccccaaatttttcaataac 10825

RESULT 3

AAC68427

ID AAC68427 standard; DNA; 10825 BP.

XX AAC68427;

AC AAC68427;

XX 21-FEB-2001 (first entry)

DT 21-FEB-2001 (first entry)

XX Human, hereditary hemochromatosis 24d2 mutation DNA.

DE, Human, hereditary hemochromatosis 24d2 mutation DNA.

XX HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ds.
XX Homo sapiens.
XX US6140305-A.
PN 31-OCT-2000.
XX 04-APR-1997; 97US-0834497.
XX 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DF, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX WPI; 2001-006341/01.
DR P-PSDB; AAB36871.
XX New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX Disclosure; Fig 3; 108pp; English.
XX The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 other;

Query Match 100.0%; Score 10823; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTAGGTTGAGATTAATTTTAAATGTATGATTTGAATTTTGAATAATTAATTTA 60
Db 1 tctaaggttgagataaaatttttaaatgtatgattgaattttgaaaatacataattta 60
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Db 61 aatactaaagttcagatcagaacattgcgaagctactttccccaatacaaacacctt 120
QY 121 TCAGGATTTAAAAACCAAGGGGACACTGGATCAGTACTGTTTTCACAGCAGGTACTCT 180
Db 121 tcaggatttaaaacaaaggggacactggtacacctagtgtttcacaagcaggtacctt 180
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCACAGGAAGTT 240
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Db 361 atggcccgcgagccagcgccgctctctctctctgatgtcttgcagacgcgggtctg 420
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DB 3001 ggaactgttaagtttgagattccagtcagcgttccaagtggtaggcccacataggcagtt 3060
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QY	9421	GCTGCATTAATGTGGTACAAGCATTCGTCTCTGAAGGCGAGTGCTTTCAGGATACCATAT	9480
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Db	9601	acgctcatgtgagaaaagctaataaatgaatacaattaaagcgtgtatttaaataagccag	9660
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QY	9721	TATACTTTTAATACTATATTGTATTGTATCTACTGCATGATTTATTGAAAGTTCTTGTTT	9780
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Db	10321	catTTtaaatcttatcatctctgccaacacattccaacacatggtagtaagaagaa	10380
QY	10381	GGGTGACACCTGGTGGCCATAGGTAATCTACACGGTGGTCCGTGCACAGAGATGCAG	10440
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QY	10561	CTATTGTAAATTGCTGGAATCACAGGCCATTCGTGAGCTGCCTGAACCTGGGAACAACAACAG	10620
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QY	10681	TCAGAGGTACAGGCCAAAATTTCTTATGTGTGTTATTTATATATGTCATCTTATATATCTGT	10740
Db	10681	tgagaggcacaggccaataattctatgtgttatataataatgtcatctataactgt	10740
QY	10741	CAGTATTTTATAAACAATCTTCAAAACCTCACACACATTTTAAAAACAACAACCTGCTC	10800
Db	10741	cagtatTTtaaaacatcttccaacactcacacacatttaaaacaacacactgtctc	10800
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ID	AAC68428	standard; DNA; 10825 BP.
XX		
XX	AAC68428;	
XX		
DT	21-FEB-2001	(first entry)
XX		
DE	Human hereditary hemochromatosis 24dl/2 mutation DNA.	
XX		
KW	HH; hereditary hemochromatosis; chelation agent;	
KW	T-cell differentiation factor; iron overload; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	US6140305-A.	
XX		
PD	31-OCT-2000.	
XX		
PF	04-APR-1997;	97US-0834497.
XX		
PR	04-APR-1996;	96US-0630912.
PR	16-APR-1996;	96US-0632673.
PR	23-MAY-1996;	96US-0652265.
XX		
PA	(BIRA) BIO-RAD LAB INC.	
XX		
PI	Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihata	
PI	Feder JN;	
XX		
XX	WPI; 2001-006341/01.	
DR	P-PSDB; AAB36872.	
DR		
XX		
PT	New hereditary hemochromatosis gene products or polymor	

PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
XX Disclosure; Fig 3; 108pp; English.
XX
XX The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
XX Sequence 10825 BP; 29999 A; 2252 C; 2648 G; 2926 T; 0 other;
SO

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Query Match      100.0%; Score 10823; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	61	AATATCTAAAGTTTCAGATCAGAACATTTCGGAAGCTACTTTCCCAATCAACAAACCCCT	120
Db	61	aatatccaaggttcagacacgaacatttggaagctactttcccgaatcaacaacacctt	120
Qy	121	TCAGGATTTAAAACCAAGGGGACACTGGATCACCTAGTGTGTTTCACAGCAGGTACCTT	180
Db	121	tcaggatttaaaaccaaaggggacactggatcacctagtgtttcacaagcaggtaacctt	180
Qy	181	CTGCTGTAGGAGAGAGAACTAAAGTCTGAAAGACCTGTGCTTTTCACAGGAAGTT	240
Db	181	ctgctglaggagagagaaactaaagttctgaaagacctgttgcttttcaccaggaaagt	240
Qy	241	TTACTGGGCATCTCCTGAGCCTTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG	300
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Db	301	tttcccgccgcccccaaaagaagcggagatttaacggggagctgcggccagagctggggaa	360
Qy	361	ATGGGCCCGGAGCCAGGCCGGCGCTTCCTCCTGATGCTTTTGAGACACGGGTCCTG	420
Db	361	atgggcccgcttgcgtgagtcgagggcgtcgggcgaaactaggggcgcgcgggggtg	420
Qy	421	CAGGGCGCTTGTCTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGGGGGGTG	480
Db	421	cagggcgcttgcgtgagtcgagggcgtcgggcgaaactaggggcgcgcgggggtg	480
Qy	481	GAAATAACGAACACTAGCTTTTCTTCGCGCTGGGAGTTTGCTAACTTTGGAGGACCTCG	540
Db	481	gaaaaatcgaactagcttttcttcttgcgttggaggtttgctcaacttttggaaggaacctg	540
Qy	541	TCAACCCCTATCCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTAGGAGTGC	600
Db	541	tcaacctctatccgcaagccctctccctaattctgcgtccagaacccgtgagggaagtc	600
Qy	601	CTACCACTGAACGCAGATAGGGTCCCTCGCCCCAGGACCTGCCCCCTGCCCGGCTGT	660
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Qy	661	CCCGCTCTGGGAGTGACTTTTGGAACCGCCCACTCCCTTCCCCCACTAGAAATGCTTT	720
Db	661	cccgctctcggaagtgaacttttggaccgcccactcccttcccccaactagaatgcttt	720
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QY	3181	TGGTGAACCCCATGCTCACTAAATAACAAAAATTAGCCCTGGTGTGTGGCGCACCGCT	3240
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Db	3241	atagtcccaggttttcaggaggcttaggtaggagaatcccttgaaccaggaggtgcagg	3300
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QY	3361	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	3420
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Db	3421	tctaattgccctgagccacaacctcctgagttcaactaccatggctagacacacaccttaac	3480
QY	3481	ATTTCTTAGAATCACAGCTTTAGTGGAGTCTGTCTAATCATCAGTATTGGGAATAGGAT	3540
Db	3481	attttcagaatccaccagctttagtgagtcgtctctaattcatgtagttatgggaataggat	3540
QY	3541	CTGGGGCAGTGAGGGGTGGCAGCCACGCTGGCAGAGAAAACGACACAAAGAAAAGAGC	3600
Db	3541	ctgggggcagtgaggggggtggcagccaagtgggcagagaaaagcacacaaggaagaagc	3600
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Db	3601	accaggactgtcaatatggagaagaagcaggactgcaactcacccttcaaaaatgagga	3660
QY	3661	CCAGACACAGCTGATGGTATGATGTTGATCGAGGTGTGGAGCCTCAACATCTGTCTCC	3720
Db	3661	ccagacacagctgattggtatgattgattgacaggtgtgtggagcctcaactcgtctccc	3720
QY	3721	CTCTACTACACATGTTAAGCCCTTGCTCTGCTCCAGGTTTCACACTCTCTGACACTA	3780
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QY	3781	CTCTTCTAATGGGTGCCTCAGACAGGACCTTGGCTTTCTCTTGTTCGAACTTTGGGCTA	3840
Db	3781	cctctctaatgggtgcctcagcaggacaccttggctcttcttctgtttgaagcttgggata	3840
QY	3841	CGTGGATGACCAGCTCTTGGTGTCTATGATNATGAGAGTCGCGGTGGAGCCCGAAC	3900
Db	3841	cg tggatgaccagcttctcgtttctctatgtagtgagagtcgcogtgtggagcccgaaac	3900
QY	3901	TCCATGGGTTTCCAGTATAGAAATTTCAAGCCAGATGGCTGAGTGCAGAGTCTGAA	3960
Db	3901	tccatgggtttccagtagaatttcaagccaagatgtggcctgcagctgagtcagagctctgaa	3960
QY	3961	AGGTGGGATCACATGTTCCATGTTGACTTCTGGACTATTATGSAAAATCACAAACACAG	4020
Db	3961	agggtggaatcacatgttcaactgttgaacttcttggactattatggaaaa tcaacaaccacag	4020
QY	4021	CAAGGATATGTGAGAGGGGCGCTCACCTTCTCAGGTTGTCTCAGAGCTTTTCACTTTTC	4080
Db	4021	caaggatatgtggagagggggcctcacctctcaggttgttcagagcttttcaatcttttc	4080
QY	4081	ATGCATCTTTGAAGAAACAGCTTGAAGTCTCAGGCTCTTGTGGGAGCAGGGAAGGAAAG	4140

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Qy	1441	TGTAGCACAGTTCCTGTGGGTACACGCCGCCCTCACACAGACACTTTTGAGTTTGCSTA	1500
Db	1441	tgtagcacagttcttgtgtgggtacaacgcccgccccaagcagcactcttgagttcttggta	1500
Qy	1501	CTAGCGTATTCACATTTTACACATGACAAGAATGAGGCATGGCAGCGCTGCTTCCTGG	1560
Db	1501	ctacgtgatccacattttaacatagcagaagaatgaggcatggcacggcctgcttcctcg	1560
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Qy	1621	TATGATTTTAAACATCACACTGCATTAGAGGTTGGAATAATAAATTTTCATGTTGACCAG	1680
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Qy	1681	AAATATTTCATGTTTTCAAGTGTAAATGAGTCCCGAGCCATGTGTTGCACCTGTTCAAGCCC	1740
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Qy	1741	CAGGGAGAGACGAGGAAACAAAGTCTTTACCCCTTTTGATATTTTGCATPTTFAGTGGAGA	1800
Db	1741	caaggagagcagcaggaaaacaagcttttaecctttgatatttgcattctagtsggaga	1800
Qy	1801	GATCACAAATTAAGCAATGAGCAGAAAGATATACACATCACAGGAATCATGGGTGTTGTA	1860
Db	1801	gatcataagcaaatgagcagaagaatacaacaaccagaatacatgggtgtgtga	1860
Qy	1861	GAACACAGAAAGTCAGGCAAGTCACTCTGGGGCTGACACTTGACGACAGACATTAAGGA	1920
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Qy	1921	AATTAAGAATGATATTGACTGGGAGCAGTATTTCCAGGCAACATGAGTGGCGCTGGCAAG	1980
Db	1921	aataagaatgatattgactgggagcagtatattccacaggcaaacctgagtgggcctggcag	1980
Qy	1981	TTGGATTTAAAAGCGGTTTCTCAGCACTACTCATGTCTGTGCTGTGGGGGGGGGGGG	2040
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Qy	2101	CCTCCCTACTCATAGTGTGATAGGACATCCCCGACTCTTGACACCAAAATGTCTCT	2160
Db	2101	cctccctactcatagtgtaggagcactccccagctcttgcacaaccaaaatgtctct	2160
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Qy	2221	AATAAACAGTGTGCTGGGGAGTAGAGCCCAAGAAGTAGGTAAATGGGCTCAGAAGAGGA	2280
Db	2221	aataaacagtgatgtgcuggggaagcagagcccaagcaggtatgtgtgtgtgtgtgtgtgtgtgtgt	2280
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Qy	2341	ACAGTGATCTGCACAGGCTTTTAAAGATTTGCTCTGGCTGCTATGTGGGAAGCAGATG	2400
Db	2341	acagtgatctgtcacaggctttttaaagattgtctgtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2400
Qy	2401	AAGGGACACAGTAAAGCAGGGGCCCGACCGAGGAGCTGTTACACAGTCCAGGCAAG	2460
Db	2401	aagggaagcaacagttaaagaagggagcccaagcccaagcagtcgttacaagccccaggcag	2460
Qy	2461	AGGTAGTGGAGTGGGTGGGAACAGAAAGGAGGAGTGACAAACCATGCTCTCTCTGAA	2520

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DB	4691		
DB	4691	tgagacgacacaaagtcaggggttaatttcttcttccatgcatatggctcaaaagga	4740
QY	4741	GTGTCTATGGCCCTCTGCTTTTATTTAAACCAATATCTTTTGTAATTTATACCTGTTAA	4800
DB	4741		
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QY	4801	AAATTCAGAAATGTCAAAGCCGCGACGGTGCTCACCCCTGTATATCCAGCACTTTGGG	4860
DB	4801		
DB	4801	aaattcagaaatgtaaggccgggcaagggtgcacctgtaatccagcaactttggg	4860
QY	4861	AGGCCGAGGCGGTGTCTACAAGTTCAGAGTTTGAGACCAAGCCTGACCAACATGTTGAA	4920
DB	4861		
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DB	4921		
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QY	5161	ATATCAAGTGAAGCCACTTATCAGAGTAGAAGAACTCTTTAGGTAAAGTTCTTTTCAT	5220
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DB	5161	atatcaagtggccacttatcagagtagaagaaacctttagggttaaaagttcttctcat	5220
QY	5221	AGACATATGACAAATATTCACCTGAGCTACCTATCTTTACAAGTCCCGTTCTTTATACATGC	5280
DB	5221		
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DB	5281		
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DB	5461		
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DB	5521		
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DB	5581		
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DB	5701		
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Qy	6541	ATCACAATCAGCTGGGATCAAGATAGCCTTCTGATCTTTGAAGCAGAAAGCTGGATTCCA	6600
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Db	6601	ttaggtgaggtgaagatgatgggagctcacacagacggagcaaccatgccaagttagga	6660
Qy	6661	GAGTATAGGCATACTGGGAGATTAGAAATAATTCTGTACCTTAAACCTGAGTTGGGT	6720
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Qy	6721	AGCTATCACTACCAATATTATGCAATTTTACCCCTGAAACATCTGTGGTGTAGGGAAGA	6780
Db	6721	agctatcactaccaattatgcatttctaccacctgaacatctgttgggtaggggaaaaaga	6780
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Db	6781	gaatcagaagaagcagctcatcagagtcacaaggggtcttcttgggatatgggttataaga	6840
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WO200058515-A1.

05-OCT-2000.

24-MAR-2000; 2000WO-US07982.

26-MAR-1999; 99US-0277457.

(BILL-) BILLUPS-ROTHENBERG INC.

Rothenberg BE, Sawada-Hirai R, Barton JC;

WPI; 2000-647244/62.

Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -

Example 1; Page 21-28; 55pp; English.

The present sequence represents the human histocompatibility iron loading (HFE) gene. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number U60319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder e.g. haemochromatosis, or a genetic susceptibility to develop it.

Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;

Query Match 99.4%; Score 10759.8; DB 21; Length 12146;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 10812; Conservative 0; Mismatches 9; Indels 8; Gaps 4;

QY 1 TCTAAGGCTGAGATAAAATTTTAAATGTATGATGAAATTTTGAATAATCATAAATATTTA 60
DB tctaaagttgagataaaaatttttaaatgtatgattgaattttgaaatcataaatattta 948
QY 61 AATATCTAAAGTTCAGATCAGAACATTTCGAAGCTACTTTCCCAATCAACACACCCCT 120
DB aatatctaaagttcagatcagaacatttgcgaagctactttccccaatcaacacacccct 1008
QY 121 TCAGGATTTAAAAACCAAGGGGACACTGTGATCACCCTAGTGTGTTTCACAAGCAGGTACTCT 180
DB tcaggattttaaaacccaagggggacactggatcacctagtgtttccacaagcaggtacctt 1068
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCATAAGACCTCTGCTTTTACACAGGAAGTT 240
DB ctgctgtaggagagagagaaactaaagtctgaaagacctgttgcctttccaccaggaagt 1128
QY 241 TTACTGGGCATCTCTGAGCCTAGGCCAATAGCTGTAGGGTGTACTTTCTGGAGCCATCCCG 300
DB ttactgggcattctctgagcctagcctaggaatagctgtagggtgacttctggagccatcccc 1188
QY 301 TTTCCCGCCGCCCAAAAGAGCGAGATTAAACGGGACGTGCGGCACAGAGCTGGGAA 360
DB tttcccgccgcccaaaagagcgagatttaacggggaagtcgagagtcggggaa 1248
QY 361 ATGGCCCCGGAGCAGCGCGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGGCTCTG 420
DB atggccccggagccagggcgcttctcctctgatgctcttttgagaccgcggtcctg 1308
QY 421 CAGGGCGCTTGTGCTGTAGTCCGAGGGCTGCGGGCGAACTAGGGCGCGGGGGGGTG 480
DB cagggcgcttgtgctgtgagtcgagggcggtcggggaactagggcggtgggggtg 1368
QY 481 GAAAAATCGAAACTAGCTTTTCTTCGCTTGGAGTGTGCTAACTTTTGAGAGACCTGC 540
DB gaaaaatcgaaactagcttttcttcgcttggagcttcttctgctggagcttctgagaccctgc 1428
QY 541 TCAACCTATCCGCAAGCCCTCTCCCTACTTTCTGCTCCAGACCCCGTGAGGAGTGC 600
DB tcaacccaatccgcaagccctctccctactttctgctccagaccctgtgagggagtgc 1488
QY 601 CTACCACTGAAGTGCAGATAGGGTCTCTGCGCCCGAGAGCTTGCCTCCCTCCCGGGCTGT 660
DB ctaccactgaactgcagataggggtccctcgcccgccaggaactgccccctccccggctgt 1548
QY 661 CCCGGCTCTGGGAGTGACTTTTGGAAACCGCCACTCTCCCTTCCCCCAACTAGATGCTTT 720
DB cccggctctgcggagtgacttttggaaacccgcccactcccttcccccaactagatgcttt 1608
QY 721 TAAATAAATCTCGTAGTTCCTCACTTGTAGCTGTAGCTAAGCCTGGGGCTCCTTTGAACCTGG 780
DB taataaaatctcgtagttcctcaacttgagctgagctgaagcctggggtccttgaacctgg 1668
QY 781 AACTCGGGTTTATTTCCAAATGTGAGCTGTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 840
DB aactcgggtttatttccaatgtcagctgtgcagtttttccccagtcattcccaaacagg 1728
QY 841 AAGTTCTTCCCTGAGTGCTTCCCGAGAAAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900
DB aagttcttccctgagtgcttgcggagaaagcctgagcaaacccacagcaggtccgcacagg 1788
QY 901 GGTTCACCTCAGAAAGAAATGCTTGGGGGTGGGGCGCGAAAGAGTGGCGTGGGGA 960
DB ggtttcacctcagaacgaatgcgttggcggtggggcgcgaaagagtggtgtggga 1848
QY 961 TCTGAATCTTCACCAATTCACCCACTTTTGGTGAGACCTTGGGGGTGGAGGTCTCTAGGGT 1020
DB tctgaattcttcaccatttccaccacttttggtagacctgggggtggaggtctctaggt 1908
QY 1021 GGGAGGCTCTGAGAGAGGCTTACTCGGCTTTTCCCTGCTTGGCAATTTGTTCTTTT 1080
DB gggaggctcctgagagagggcctacctcggccttccccactcttcccaattgttctttt 1968
QY 1081 GCCTGGAAAAATAAGTATATGTTAGTTTGAACGTTTGAACGTTTGAACGTTTGAACGTTTGAACG 1140

|||||
6345 taggacaaaaaggtgtctctctgtagctgtgttttttctgaaagggtatttctctc 6404
QY CTCCAACCTATAGAAAGGAAAGTCCAGTCTCCAGTCTTCCTGGCAAGGTAACAGAGTCCCC 5576
Db ctccaaacctagaaaggaagtgaagtctccagctctctcctggcaagggttaacagatcccc 6464
QY TCTCCTCATCCTTCCTTCCTTCCTCAAGTGCCTCCTTCCTGGTGAAGGTGACACATCATGT 5636
Db tctctcatctcttctcttctctgtcaagtgcctctcttgggtgaaggtgaacatactgt 6524
QY GACCTCTTCAGTGACCACTCTACGGTGTGGGCTTGAACACTACTACCCCCAGAACATCAC 5696
Db gacctctcagtgaccactctacgtgtcgggcttgaactactaccocagaaacatcac 6584
QY CATGAAGTGGCTGAGGATTAAGCAGCCCAATGGATGCCAAGGAGTTCGAACCTTAAGACCT 5756
Db catgaagtggctgaagataaagcagoccaa tggatgcgaaggagttcgaacctaaagacgt 6644
QY ATTGCCCAATGGGATGGGACCTACCAGGCTGGATAACCTTGGCTGTACCCCTGGGGA 5816
Db attgcccaatgggaatgggacctaccaggctggataaaccttggctgtaccctctggga 6704
QY AGACGAGAGATATAGTNCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTGAT 5876
Db agagcagagataacgtgcaggtggagcaccagcctggatcacccctcatgtgat 6764
QY CTGGGGTATGTGATGATGAGCGCAGAGCTGAGAAATCTATTGGGGTTGAGAGGAG 5936
Db tgggggtatgtgactgtagagaccaggagctgagaaaaactatctgggggttgagaggag 6824
QY TGCTGAGGAGGTAAATPATGGCAGTGAGATGAGATCTGCTTTGTAGGGGTGGCT 5996
Db tgcctgaggagtaattatggcagtgagatgagatctgtcttctgttagggatgggt 6884
QY GAGGTTGGCAATCAAGGCTTTAACTTGCTTTTCTGTTTAGGCCCTCACCGCTCTGC 6056
Db gaggggtgcaatcaaggctttaacttgcctttctgtttagagccctcacctctcgtg 6944
QY ACCCTAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTTCGTCATCTTGTTCATTGGA 6116
Db accctagtcattgagtcacatcagtggaatlgctgttttctgtctcatctgttcattgga 7004
QY ATTTTGTTCATAATTAAGAAAGGACGAGGTTCAGTGAGTAGAGAAAGGGGAAGT 6176
Db attttgttcaaatatlaaggaaaggcaggggttcaaagttaggaacaaagggggaagt 7064
QY CTCCTAGTACCTCTGCCCCAGGCGACAGTGGGAAGGGCGCAGAGGGGATCTGGCATCCA 6236
Db ctcttagtacctctgccccaggggcacagttg99gaagagg99gaactg99catccca 7124
QY TGGGAAGCATTTTCTCATTTATATCTTTGGGACACACGAGCTCCCTGGGAGACAGA 6296
Db tgggaagcattttctcatcttatcttcttgggagacaccagcagctccctgggagacaga 7184
QY AAATTAATGGTTCTCCCGAAGTAAAGTCTTAATTAACAACAACTCTCAGAGCACCTA 6356
Db aaaataatggttctccagagaagaagtctctaaattcaacaacaacatctcagagaccta 7244
QY CTATTTTCAAGAGCTGTTTAAAGTAGTACAGGGGCTTTGAGGTTGAGAAAGTCACTGTGG 6416
Db ctattttgcaagagcgtcttaaggtagtacaaggggctttgaggttgagaagtcactgtgg 7304
QY CTATTCTCAGAACCCAAATCTGGTAGGGAATGAAATGTATAGCAAGTAAATGTAGTTAAA 6476
Db ctattctcagaacccaatactcgtgaggaatgaaatgtagcaagtataatgtagttaa 7364
QY GAAGACCCCATGAGGTCTTAAGCAGGACGCAAGCAAAATGCTTAGGGTGTCAAGAGAAAG 6536
Db gaagaccccatgaggtctcgaagcaggcagggaagcaaatgcttaggggtgcaagggaag 7424
QY AATGATCACATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAAGCTGGAT 6596
|||||

Db 7425 aatgatcacattcagctgggagatcaagatagcctctctggtatcttgaaggagaaagctgagat 7484
QY TCCATTAGGTGAGGTTGAAGATGATGGAGGTCTACACAGACGGAGCAACCATCCCAAGT 6656
Db tccattagtgaggtgaagatgatggaggtctacacagacggagcaacccatgccaagt 7544
QY AGGAGAGTATAGGCATVACTGGGAGATTAGAAATAATTTACTGTACCTTAACCCGTGAGTTT 6716
Db aggagagLataaggcatactaggagattagaaaLaattactgtaccttaacctgagttt 7604
QY GCGTAGCTATCACCTACCAATTTATGCATTTCTACCCCTGAACATCTCTGTGTGAGGAA 6776
Db gcttagctcatcactaccaaattatgcatcttcccccgaacatctgctggctgag99aa 7664
QY AAGAGAATCAGAAAGAACCCAGCTCATACAGAGTCCAAAGGCTCTTTTGGGATATTGGGTT 6836
Db aagagaatcagaagaagaccagctcatcacagagtcaccaagggtcttttgggatatggggt 7724
QY ATGATCACTGGGGTGTCAATTTGAAGGATCCTTAAGAAAGAGGAGCACCGATCTCCCTTATAT 6896
Db atgatacactgggtgtcatctgaaggatcctaagaaaggagaccacgactcctccttat 7784
QY GGTGAATGTGTTTAAAGAAGTTAGATGAGAGGTGAGGAGACCCAGTTAGAAAAGCCAAATAA 6956
Db ggctgaatgtgttcttaagaagttagatgagagggtgagagagaccaggttagaaagccaataa 7844
QY GCATTTCCAGATGAGAGATAATGTGTTTGAATCCAAATAGTGCCCGAGGTCTAAATTGAG 7016
Db gcaattccagatgagagataaagggtctctgaaatccaatagtgccccaggtctaaattgag 7904
QY ATGGGTGAATGAGAAATAAGGAAGAGAGAGAGAGAGAGTGTGCCTAGGTTTGTGAT 7076
Db atgggtgaatg99gaataaaggaaagagagagagagagatg99gcctcag99tttctgtat 7964
QY GCCTCTTTCTGGGTCTCTTGTCTCCACAGGAGGAGCCATGGGCACTACGCTCTTAGCTG 7136
Db gcocttctctgggtctcttctgtctccacaggaggagccatggggaactacgtcttagctg 8024
QY AACGTGAGTGACACGCGCTGCAGACTCAGTGTGGGAGGAGACAAAACCTAGAGACTCA 7196
Db aacgtgagtgacacgcagcctgcagactcaactgtg99gaagagagacaaactagagactca 8084
QY AAGAGGGAGTGCAATTTATGAGCTCTTCATGTTTCAGGAGAGAGATTGAACCTAAACATAGA 7256
Db agag99gaagtcgatttatgagctctctcatgtttcaggaagagaggttgaacctaaacataga 8144
QY AATGCGCTGACGAACCTCCTTGATTTTAGCCTTCTCTGTTCATTTCTCCTCAAAAAGATTTCC 7316
Db aattgctgcagcaactccttgatttagcctctctctgttcttctctcaaaaagatttcc 8204
QY CCATTTAGGTTTCTGAGTTCCCTGCATGCGGGTGATCCCTAGCTGTGACCTCTCCCTCGA 7376
Db ccatttaggttctcagttcctgcagtcgcggttgatccctagctgtgacctctccctgga 8264
QY ACTGTCTCTCAAGCTCAAGCTGCATCTAGAGGCTTCTCTTCATTTCTCCGTCCACCTC 7436
Db actgtctctca tgaacctcaagctgcactagaggtctcttcatcttctcctcagctcacctc 8324
QY AGAGACATACACCTATGTCAATTTTCAATTTTCTCCTATTTTGGAGAGGAGCTCCTTAAATTTGG 7496
Db agagacatacaccta tgcatttcttcttcttcttatttttggagaggagactctcttaaatgtg 8384
QY GGCACATTACATGATTCATTTTAACATCTCAGAAAGCTTTGAACCTGGGAGCTGGCTAG 7556
Db gggacttatcatgattctatttaaca tctgagaaaagcttctgaacctctg99gcgtg99cag 8444
QY TCATAACCTTACCAGATTTTACACATGATCTATGATTTTCTGGACCCGTCAACTTTT 7616
Db tcataaccttacagatttttacacatgfatctatgcatcttctgagaccgttcaacttt 8504
QY TCTTTGAATCTCTCTGTGTGTACCCAGTAACTCATCTGTACCAAGCCCTTGGGATTT 7676
Db tectttgaatcctctctctgtgttaaccagtaactcatctgtcaccaagccttgggagatt 8564

Qy	7677	CTTCCATCTGATTGTGATGTGCTCCACAGCTATGAGGCTGTACACTGCACGAATGGA	7730
Db	8565	cttccatctgattgtgatgttgagtgccagagctaTgaaggtctgtacactgcacgaatggga	8624
Qy	7737	AGAGGCACCTGTCCCGAGAAAAGCATCATGGCTATCTCTGGGTAGTATGATGGGTGTTTT	7796
Db	8625	agaggcaacctgtcccgagaaaagcatcaTggctatctgtggttagtaTgaTgggtgtttt	8684
Qy	7797	TAGCAGGTAGAGAGCGCAAAATATCTTGAAGGGGTTGTGAAGAGGTGTTTTTCTAATTTGGC	7856
Db	8685	tagcaggtagagagcgcaaatatcttgaaggggttggaagagggttttttctcaattggc	8744
Qy	7857	ATGAAGGTGTCATACAGATTTTGCAAAAGTTTAATGTGCTTCATTGTGGATGCTACHTCTA	7916
Db	8745	atgaaggtgtcaTcacagatttgcaaaagtctaaTggtgcttcaatttgsgaTgctacacta	8804
Qy	7917	GTATTCCAGACCTCGAAGATCAATAATTTTCTACCTGGTCTCTCTGTGTCTTGATAAAT	7976
Db	8805	gtattccagacctgaagaatcacaaataatttctaccTggtctctctctgttctgataat	8864
Qy	8037	CTTACATGCAATTACTCGCAGTCTCTTACAAATAATCTATGAGTAGGTACTATTATCC	8096
Db	8925	cttacaTgcatctgcaTgcatctcttacaataattctatgatatggttactattatcc	8984
Qy	8097	CCATTCTCTTTTAAATGAAGAAGTGAAGTAGGCCGGGCACGGTGGCTCACGGCTGTAA	8156
Db	8985	ccattctctttttaaataagaagaagtgaagttaggcgggcaggtggtctcaTgcctgtaa	9044
Qy	8157	TCCCAGCACTTTGGGAGGCCAAAGCGGGTGTATCAGAGGTCAGAGATCGAGACCAATCC	8216
Db	9045	tcccagcaactttggggagggccaaagcgggtggatcacagaggtcagTgagatcgagaccatcc	9104
Qy	8217	TGGCTAACATGTGTAAACCCCATCTCTAATAAATAACAAAAATTAGCTGGGGCTGGTG	8276
Db	9105	tggtcaacatggtgaaccccatctctaataaaaaatacaaaaaattagctTgggctgggtg	9164
Qy	8277	GCAGAGCCTGTAGTCCCAGCTACTCGGAAGGCTGAGCGCAGGAAATGGCATGAACCCAG	8336
Db	9165	gcagagcctgtagtcccgactactcTggaaggtcagTgaggaagaaTggcatgaaccag	9224
Qy	8337	GAGCGAGAGCTTGCAGTGACCGAGTTTGGCCACTGCACATCCAGCCTTAGTGTACACAGT	8396
Db	9225	gagggcagagctgtcagTgagcgcgagttTgcgcactgcactcccgactaggtgacagagt	9284
Qy	8397	GAGACTCCATCTCAAAAAATAAAAAATAAAAAATGAAAAAAGAAAGAGTGA	8456
Db	9285	gagactccatctcaaaaaataaaaaataaaaaataTgaaaaaadaaaagaaTgca	9344
Qy	8457	AGTATAGATATCTCATAGTTTGTTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTG	8516
Db	9345	agTatagagtatctcatagtTtTgtcagTgatagaacaggTttcaaaactcagTcaactctg	9404
Qy	8517	ACCGTTTGTATACATCTCACACACCACACTACATTCAGTATGTTAGATGCCTAGATAAATAG	8576
Db	9405	accgTttgatatactcagacaccactacattcagtagtttagatgctcagataTaaatag	9464
Qy	8577	AGAAGGAAGGATGGCTCTTCTCTGTCTCATTTGTTTCTTCTGTAGTGAGCTTGAATC	8636
Db	9465	agaagaagagagatggctctctctgttctcatgtgtttctctgtgaatgagctctgaatc	9524
Qy	8637	ACATGAAGGGGAACAGCAGAAAAACCAACTGATTCCTCAGCTGTCAATGTTTCTCTTTAAA	8696
Db	9525	acatgaaggggaacagcagaaaaaaccaactgacTcctcagctgtcatgtttctctttaa	9584
Qy	8697	AGTCCCTGAAGGAGGTCTCGAATGTGACTCCCTTGCTCTCTCTGTGTGCTCTCTTTGGCA	8756
Db	9585	agTccctgaaggaagTcctctgaaTgtgactcccttgcctctgtTgctccttttagca	9644

[illegible]

Db 10725 attctcttaacatttgccttaacggaattatttcaattcaactggtgtagccgaattaatcg 10784
Qy 9897 TGTTCCTTCACTAGGGACATTGTCGTCTAAGTTCTTAAGACATTGGTTATTTTACCAGC 9956
Db 10785 tgtttcttcaacttagggacaattgctgctaagttgtaagacaattggttatttaccagc 10844
Qy 9957 AAACCACTCTGAAGCATATGACAAATTAFTTCTCTTAATATCTTACTACTACTGAAG 10016
Db 10845 aaaccattctgaaagcatatgacaaaattattctctttaataattactactactgaaag 10904
Qy 10017 CAGACTGCTATAAGGCTTCACTTACTCTCTCTACCTCATAGGAATATCTTACAATTAAT 10076
Db 10905 cadagtctataaggtctcaactcacctctcaactcataaggaaatggtacaattaat 10964
Qy 10077 TATTAGTAAAGCATTTGTTTATTATTTGGTTTATTTCACCTGGCTGAGATTTCAGAAAA 10136
Db 10965 tattagtaagcattgtttttatatagttttatttcaacctggctgagatttcaagaaa 11024
Qy 10137 CACCCAGTCTTACAGTACACATTCTACTTAACATACATTTACTTAACATCAGCAACTGTG 10196
Db 11025 caccacgctctcacagtaaacatttctactaacacatttactaaacatcagcaactgtg 11084
Qy 10197 GCCTGTTAAATTTTAAATAGAAATTTTAAGTCTCTCATTTCTTCGGTGTTTTAAAGC 10256
Db 11085 gccgttcaattttttaaataagaaatttcaagtcctcatttcttcttcggtgtttttaaagc 11144
Qy 10257 TTAATTTTCTGGCTTTATTCATAAATTTCTTAAGGTCAACTACATCTGAAAAATCAAGA 10316
Db 11145 ttaattttctgctttattcataaattcttaaggtcaactacatttgaataatcaaga 11204
Qy 10317 CCTGCATTTTAAATCTTATTACCTCTGCGCAAAACCATTCACAAACCATGGTAGTAAG 10376
Db 11205 cctgcattttaaattcttattcctctgcaaaacatttcacaaacccatggtagtaag 11264
Qy 10377 AGAAGGTGACACCTGTGCGCATAGTAAATGTACACAGTGTGTCGGTGACACAGAT 10436
Db 11265 agaagggtgacacctgggtgccaaggttaaatgaccacggtggtccggtgaccagagat 11324
Qy 10437 GCACGCTGAGGGTTTTCCTGAAGTAAGGAATAAAGAAATGGGTGGAGGGCGTGCACT 10496
Db 11325 gcagcgtgagggtttctcctgaaggtaaaaggaataagatggtgagggcgctgcaact 11384
Qy 10497 GGAATCACTTGTAGACAAAGCCCTGAAAATTTGAGAAAAACAACAGAAACTACTTA 10556
Db 11385 ggaatacactgttagaagaaagccctgaaaatttgagaaaaacaagaactactta 11444
Qy 10557 CCAGCTATTTGAATTGCTGAATCACAGGCCATTGTGCTGAGCTGCCTGAACCTGGGAACACA 10616
Db 11445 ccagctatttgaattgctggaatacacaagccattgctgagctgcaactgggaacaca 11504
Qy 10617 ACAGAAGGAAACAAACCACTCTGTAAATCATTTGAGTCAAGTACAGCAGGTGATTGAGGA 10676
Db 11505 acagaagaaaaaacaaccactctgataatcatgagtcagtcagcaggtgattgagga 11564
Qy 10677 CTGCTGAGAGGTACAGGCCAAAATTTTATGTTGTTATTAATGTCATCTATAATA 10736
Db 11565 ctgctgagaggtacagcccaaaattcttatgttgattataataatgtcatcttaata 11624
Qy 10737 CTGTCAGTATTTTATAAACAATTTCTCACAAACTTCACACACATTTTAAAAACAAACACTG 10796
Db 11625 ctgctcagttatttataaaacattcttcacaaacttcacaaacttcacacacatttaaaaaaacactg 11684
Qy 10797 TCTCTAAATCCCAAAATTTTTCATAAAC 10825
Db 11685 tctctaaatccccaatttttctataaac 11713

RESULT 7
AAV57903/c
ID AAV57903 standard; DNA: 237326 BP.
XX
XX AAV57903;
AC

XX 21-DEC-1998 (first entry)
DT Hereditary haemochromatosis subregion from an HH affected individual.
XX
DE Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
XX diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW type 1 sodium transport gene; ss.
XX
OS Homo sapiens.
XX
XX WO9814466-A1.
PW
XX 09-APR-1998.
PD
XX 30-SEP-1997; 97WO-US17658.
PF
XX 07-MAY-1997; 97US-0852495.
PR
XX 01-OCT-1996; 96US-0724394.
XX
XX (PROG-) PROGENITOR INC.
XX
XX Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;
PI Tsuchihashi Z, Wolff RK;
XX
XX WPI: 1998-240014/21.
DR
XX Hereditary haemochromatosis gene products - used to develop products
PT for the diagnosis and treatment of hereditary disorders in iron
PT metabolism
XX
XX Claim 1; Fig 9; 209pp; English.
PS
XX The present invention describes hereditary haemochromatosis gene
CC products from the human haemochromatosis gene. The present sequence
CC represents a hereditary haemochromatosis subregion from an hereditary
CC haemochromatosis (HH) affected individual. Also described is a
CC method to determine the presence or absence of the common hereditary
CC haemochromatosis (HFE) gene mutation in an individual comprising:
CC (a) providing DNA or RNA from the individual; and (b) assessing the
CC DNA or RNA for the presence or absence of a haplotype or genotype where
CC the presence or absence of the haplotype genotype indicates the likely
CC presence of the HFE gene mutation in the genome of the individual. The
CC HFE gene sequences from the present invention can be used to develop
CC products for use in the diagnosis and treatment of HFE. The present
CC invention also describes BTF genes, which are homologues of the milk
CC protein butyrophilin (BT), and can be used in the production of agonists
CC and antagonists of BT function. Also described are: (1) a RoRet gene
CC which can be used to develop products for the study, diagnosis and
CC treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC which are homologues of a type 1 sodium transport gene, and can
CC similarly be used for hypophosphatemia.
XX
XX Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;

Query Match 98.9%; Score 10707; DB 19; Length 237326;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 10779; Conservative 0; Mismatches 42; Indels 8; Gaps 4;
Qy 1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTGAAAATCATAAATATTTA 60
Db 47101 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTGAAAATCATAAATATTTA 47042
Qy 61 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAACACCCT 120
Db 47041 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAACACCCT 46982
Qy 121 TCAGGATTTAAAAACCAAGGGGACACTGGATCAGCTAGTGTTCACAAGCAGGTACCTT 180
Db 46981 TCAGGATTTAAAAACCAAGGGGACACTGGATCAGCTAGTGTTCACAAGCAGGTACCTT 46922

Db 40385 GCTTAGCTATCACTACCAAAATTATGCAATTTCTACCCCTGAACATTGGTGGTAGGGAA 40326
 QY 6777 AAGAGAATCAGAAAGACCGCTCATACAGAGTCCAAGGTCCTTTTCGSGATATGGTT 6836
 Db 40325 AAGAGAATCAGAAAGACCGCTCATACAGAGTCCAAGGTCCTTTTCGGAATAATGGGTT 40266
 QY 6837 ATGATCACTGGGGTGTCAATTGAAGGATCCTAAGAAAGGAGGACCAACGATCTCCCTTATAT 6896
 Db 40265 ATGATCACTGGGGTGTCAATTGAAGGATCCTAAGAAAGGAGGACCAACGATCTCCCTTATAT 40206
 QY 6897 GGTGAATGTGTGTTAAGAAGTTAGATGAGAGGTGAGAGAGCCAGTTAGAAGCCAATAA 6956
 Db 40205 GGTGAATGTGTGTTAAGAAGTTAGATGAGAGGTGAGAGAGCCAGTTAGAAGCCAATAA 40146
 QY 6957 GCAATTTCCAGATGAGAGATAATGTTCTTGAAATCCAAATAGTGCCAGGTCTAAATTGAG 7016
 Db 40145 GCAATTTCCAGATGAGAGATAATGTTCTTGAAATCCAAATAGTGCCAGGTCTAAATTGAG 40086
 QY 7017 ATGGGTGAATGAGGAAATTAAGGAAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGAT 7076
 Db 40085 ATGGGTGAATGAGGAAATTAAGGAAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGAT 40026
 QY 7077 GCCTCTTTCCCTGGGTCTCTGCTCCACAGGAGGAGCCATGGGCACCTAGCTCTTAGCTG 7136
 Db 40025 GCCTCTTTCCCTGGGTCTCTGCTCCACAGGAGGAGCCATGGGCACCTAGCTCTTAGCTG 39966
 QY 7137 AACGTGAGTGACACGACCGCTGCAGACTCACTGTGGAAAGGAGACAAACTAGAGACTCA 7196
 Db 39965 AACGTGAGTGACACGACCGCTGCAGACTCACTGTGGAAAGGAGACAAACTAGAGACTCA 39906
 QY 7197 AAGAGGAGTGCATTTATGAGCTCTTCATGTTTCAGAGAGAGTTGAACCTAAACATAGA 7256
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RESULT 8

AAL36747

ID AAL36747 standard; DNA; 5749 BP.

XX AAL36747;

XX

XX 08-JAN-2002 (first entry)

XX

Human musculoskeletal system related polynucleotide SEQ ID NO.3112.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.

OS	Homo sapiens.		
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PN	WO200155367-A1.	PR	27-SEP-2000; 2000US-0235834.
XX		PR	27-SEP-2000; 2000US-0235836.
PD		PR	29-SEP-2000; 2000US-0236327.
XX	02-AUG-2001.	PR	29-SEP-2000; 2000US-0236367.
XX		PR	29-SEP-2000; 2000US-0236368.
PF		PR	29-SEP-2000; 2000US-0236369.
XX	17-JAN-2001; 2001WO-US01338.	PR	29-SEP-2000; 2000US-0236370.
XX		PR	02-OCT-2000; 2000US-0236802.
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PR	28-JUN-2000; 2000US-0214886.	PR	20-OCT-2000; 2000US-0241787.
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PR	01-SEP-2000; 2000US-0229387.	PR	08-NOV-2000; 2000US-0246532.
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PR	14-SEP-2000; 2000US-0232399.	PR	08-NOV-2000; 2000US-0246532.
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PR	14-SEP-2000; 2000US-0232401.	PR	08-NOV-2000; 2000US-0246532.
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PR	21-SEP-2000; 2000US-0234223.	PR	08-NOV-2000; 2000US-0246532.
PR	21-SEP-2000; 2000US-0234274.	PR	08-NOV-2000; 2000US-0246532.
PR	23-SEP-2000; 2000US-0234997.	PR	08-NOV-2000; 2000US-0246532.
PR	23-SEP-2000; 2000US-0234998.	PR	08-NOV-2000; 2000US-0246532.
PR	26-SEP-2000; 2000US-0235484.	PR	08-NOV-2000; 2000US-0246532.
PR		PR	05-JAN-2001; 2001US-0259678.
		XX	
		PA	(HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-451937/48.
 XX Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the musculoskeletal system including
 PT musculoskeletal cancers and also for testing and detection e.g.
 PT diagnosis
 XX
 XX Example 2; SEQ ID NO 3112; 781pp + Sequence Listing; English.
 XX
 XX The invention relates to novel genes (AAL34569-AAL37666) and proteins
 CC (AB03087-AB04109) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 XX
 XX Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;

Query Match 52.9%; Score 5724.8; DB 22; Length 5749;
 Best Local Similarity 99.8%; Pred. NO. 0;
 Matches 5740; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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 Qy 5081 TGAGATCCCATCTTAAAAAATAAAAAAAGAGAAATTCAGAGATCTCAGCTAT 5140
 Db 1081 tgagactcccatctctaaaaaataaaaaaagagaaatccagagatctcagactat 1140
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 Db 1141 catatgaatcccgagacaaaataatcaagtgtgcccacttatcagatagagaagaatccttt 1200
 Qy 5201 AGGTTAAAAATTTCTTCATAGAACATAGCAATTAATCACTGAAGCTACCTATCTTACAAG 5260
 Db 1201 a-gtataaagtctcttccatagnacatagcaataatcaactgaagctacacctatcttacaag 1259
 Qy 5261 TCCGCTTCTTTATACCAATGCTCTAGTGTGACCCAGGTGAAACTGACCATCTGTATTCA 5320
 Db 1260 tccgcttcttatacaaatgctcctcctaggttgaccacgggtgaaactgaccttctgtattca 1319
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 Db 1320 atcatcttcaatgcacataaaggcgatcttctatcagaaacaaagaaacagggtaaca 1379
 Qy 5381 GATATGTATATTTTACATGTGAGGAGACACAGCTGATCTGACTGCTCTCAAGTGACACTG 5440
 Db 1380 gatgtatatttaccatgtgaggagaacaagtgtactgctcctccaagtgaactg 1439
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 Db 1440 tgttagagtcacaatcttaggacacaaaatggtctctcctctgtagcttcttcttctctga 1499
 Qy 5501 AAAGGCTATTTCTCTCTCCCACTATAGAAGGAAGTGAAGTTCCAGTCTTCTCGGCA 5560
 Db 1500 aaaggggtatttctctctcccaactatagaagaagtgaagttccagcttctcctgggaa 1559
 Qy 5561 GGTAAACAGATCCCTCTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5620
 Db 1560 ggttaaacagatccct 1619

Qy	5621	AGGTGACATCATGTGACCTCTTTCAGTGACCACCTCTACGGTGTCCGGCCTTGAACTACT	5680
Db	1620	aggtgacatcatgtgacctcttcagtgcacctctcactggtcgggccttgaaactact	1679
Qy	5681	ACCCCGAAGACATCACCATGAAGTGGCTGAAGGATAGCAGCCCAATGGATGCCAAGGAGT	5740
Db	1680	accccgagaacatcaccatgaagtggctggaaggataagcagccaatggatgccaaaggagt	1739
Qy	5741	TGNAACCTAAAGACAGTATTGCCCAATGGGATGGACCTACCAAGGCCTGGATAACCTTTG	5800
Db	1740	tcaaacctaagaacgtattgcaccaatggggatgggaactaccagggtcgataaaccttgg	1799
Qy	5801	CTGTACCCCCTGGGAAGACGAGATATACGTNCCAGGTGGAGCACCCAGGCCTGGATC	5860
Db	1800	ctgtacccccctgggaagagcagatatagctgccaggtggaagcaccaggcctggatc	1859
Qy	5861	AGCCCTCATTTGTATCGGGTATGTGACGTGATGACGTGATGAGAGCCAGAGCTGAGAAAATCTAT	5920
Db	1860	agccctcatttgtactctggggtatlgtgactgatlgaagccaggagctgagaaaaactat	1919
Qy	5921	TGGGGTGTGAGAGGAGTGCCTCAGGAGGTAAATTATGGCAGTGCAGATCTGCTCTTT	5980
Db	1920	tgggggttgtagagaggagtcctgagagaggtaatattgycagtlgaatagagatctgctctt	1979
Qy	5981	TGTTAGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGCTTTTTTCTGTTTTAGA	6040
Db	1980	tgttaggggtgggctgagggtggaacaaggctttaactgtcttcttctgttttaga	2039
Qy	6041	GCCCTACCGTCTGGCACCCCTAGTCATTGGAGTCATCAGTGGAAATTCCTCTTTTCTGCGT	6100
Db	2040	gccctcacgctctggcacctagtcattggagtcacatgtaggaatctgtcttttgcgt	2099
Qy	6101	CATCTTGTTCATTGGAAATTTGTTTCATTAATATTAAAGGAAGGACAGGGTTCAAAGTCAGTA	6160
Db	2100	cactctgttcattggaatttgbtcaataattaaggaagaggcagggtticaagtgaagta	2159
Qy	6161	GGAAACAAGGGGAAGTCTCTTAGTACCTCTGCCCGAGGCACAGTGGGAAGAGGGGCAGA	6220
Db	2160	ggaaacaagggggaagtctctctagtacctctgcccagggccacagtggaagaggggcaga	2219
Qy	6221	GGGGATCTGGCATCATGGAGACATTTTTCATATTATTCCTTGGGACACACAGCAG	6280
Db	2220	ggggatctggcataccatgggaagcaattttctcatattataattcttggggagaccaggcag	2279
Qy	6281	CTCCCTGGGAGACAGAAAAATAATGGTTCTCCCGCAATGAAAGTCTCTAATTCAACAAC	6340
Db	2280	ctccctgggagacagaaaataatggttctccccagaaatgaagctctctaatctcaaacac	2339
Qy	6341	ATCTTCAGACACCTACTATTNTTGCANAGCTGTTTAAAGTAGTACAGGGGCTTTGAGGT	6400
Db	2340	atcttcagacacactactatttgaagagctgttttaaggtagtacagggggctttaggt	2399
Qy	6401	TGACAAGTCACTGTGCTATTCTGAAACCCCAAAATCTGSTATGGGAATCAAAATGATAGCA	6460
Db	2400	tgaagaagtcactgttgcattctccgaagcccaaaactdgttgggaatgaatgatga	2459
Qy	6461	AGTAAATGTAGTTAAAGAACCCCCATGAGTGCTTAAAGCAGGAGGAAGCAAAATGCTTA	6520
Db	2460	agtaaatgtagttlaaagaagaccccatgaggtccotlaaagcaggcaggaagcaaatgctta	2519
Qy	6521	GGGTGTCAAAGGAAGAAATGATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTT	6580
Db	2520	gggtgtcaaaggaaatgatacaattcagctggggatcagaatagactctctggaactt	2579
Qy	6581	GAAGGAGAAGCTGGATTCCATTAGGTGAGTTTGAAGATGATGGAGGTCTACACAGACGG	6640
Db	2580	gaaggagaagctggattccattaggttgaagattgaagaatgaaggaggttctcacagacgg	2639
Qy	6641	AGCAACCATGCCAAGTAGGAGAGTATATAGGCATACTGGGAGATTAGAAATTAATTTACTGTA	6700
Db	2640	agcaaccatcccagttagdagagatlaaaggcactctggaadattagaaaataactactqta	2699

Qy	6701	CCTTAACCCGTAGTTTGGGTAGCTATCACTACCAAAATTATGCATTTCTTACCCCTCGAACCA	6766
Db	2700	ccctaaacctgagtttgctgagctaTcactcaccaatatgcattcttaccacctgaaac	2759
Qy	6761	TCTGTGTTAGGAAAGAGAAATCAGAAGAGCCAGCTCATACAGAGTCCAAAGGGTCT	6820
Db	2760	tctgtgtgtagggaaagagaatcagaagaagccagctcatacagagttccaaggtct	2819
Qy	6821	TTTGGGATATTGGGTATGATNACTCGGGTGTCATTGTAAGGATTCCTAAGAAAGAGAGACC	6880
Db	2820	tttgggatatgggttatgatactcagtggttcattgaaggatccctagaagaagagacc	2879
Qy	6881	ACGATCTCCCTTATATGGTGAATGCTGTTTAAAGAGTTAGATGAGAGCTGAGGAGACCA	6940
Db	2880	acgatactccctctataTggTgaatgctgtctgaagaagttagatgagagtgagagagacca	2939
Qy	6941	GTTAAGAAGCAATAAGCATTTCCAGATGAGAGATAATGGTTCTTGAATCCAATAGTGC	7000
Db	2940	gttagaagccaataagcatattccagatgagagataatggttcttgaataccaatagtagc	2999
Qy	7001	CCAGGCTTAATTGAGATGGGTCAATGAGGAAATTAAGGAAGAGAGAGAGCAAGTAGG	7060
Db	3000	ccaagttcaaatTgagatgggtgaaTgaggaataaaggaagagagagagagcaagaTgg	3059
Qy	7061	TGCCTAGTTTGTATGCCCTTTCCTGGGTCTCTGTGTTCTCCACAGAGAGAGCCATGGG	7120
Db	3060	Tgcctaggtttgtagtcctcttctgggtctctgtctccacagagagagccatgggg	3119
Qy	7121	CACTAGCTTTAGCTGAACGTGAGTGACACGACGACGACGCTGCAGACTCACTGTGGGAAGGAGA	7180
Db	3120	cactlactcttagctgaacTgagtgacacgacgacgctgcagactcactTgtgggaaggaga	3179
Qy	7181	CAAACTTAGACATCAAGAGGAGGTGCATTTATGAGCTTTCATGTGTTTCAGGACAGAGT	7240
Db	3180	caaaacttagagactcaaaagagggagTgcatTTatgagctctcaTgtttcagagagaggt	3239
Qy	7241	TGAACCTTAAACATAGAAATTTGCCTGACGAACTCCTTGATTTTAGCGTTCTCTGTTCATTTT	7300
Db	3240	TgaacctaaacataTgaatatTgcTgacgaactcctTgatttagctctctctctgttccattt	3299
Qy	7301	CCTCAAAAGATTTCCCATTTAGTTTCTGAGTTCCTGCATGCCGGTGATCCCTAGCTG	7360
Db	3300	ccctcaaaagattTccccaatttaggtttctgagttctctgataTgcgcgTgataccctagctg	3359
Qy	7361	TGACCTCTCCCTCGAATCTCTCTCATGAACCTCAAGCTGATCTAGAGGCTTCCCTTCA	7420
Db	3360	TgacctctccctTgaaactgtctctcatgaacctaaTgcatctcatgagggcttctctca	3419
Qy	7421	TTTCTCTCGTCACCTCAGACATACACCTATGTGATTTTCATTTCTTCTATTTTGGGAAG	7480
Db	3420	tttctctcgtccactcagacatacacctatgTcatcttcaattctcatatttttggaaagag	3479
Qy	7481	GACTCCTTTAAATTTGGGGACTTACATGATTCATTTTAAATCTGAGAAAAGCTTTGAAC	7540
Db	3480	gactcctTaaattTgggggacttacaTgattcaattttaacatctgagaaaaagctttgaac	3539
Qy	7541	CCTGGACGCTGGGTATCAACCTTACCAGATTTTACACATGTATCTATGCAATTTTCT	7600
Db	3540	ccTgggacgtTgctagTcaTaaaccttaccagatttttacacatgtatctatgcatcttct	3599
Qy	7601	GGACCCGTTCAACTTTTCCCTTTGAATCCTCTCTGTGTTTACCAGTAACCTCATCTGCA	7660
Db	3600	ggacccgtTcaacttttctcttgatcctctctctgtgtttaccacagtaactcatctgTca	3659
Qy	7661	CCAAGCCTTGGGGATCTTCCATCTGATGTGATGTGAGTTGTCACAGCTATGAAGGCTGT	7720
Db	3660	ccaagcctTgggattcttccatctgattTgagtTgagttgcaagctatgaagagctgt	3719
Qy	7721	ACACTGCACGAATGGAAGAGGCACCTGCCACGAAAAGCATCATGGCTATCTGTGGGTA	7780
Db	3720	acaactgcagaaTgggaagagggcacctTcccagaaaaagcatcaTggctatctcTgTgggca	3779
Qy	7781	GTATGATGGGTGTTTATGACAGGTAGAGGAGCAATATCTTTGAAGGGGTTGTGAAGAGGT	7840

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QY 5821 CAGAGATACGTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTGATCTGG 5880
Db 41329 CAGAGATACGTGCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTGATCTGG 41270
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QY 5941 TGAGGAGGTAAATATGGCAGTGAAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 6000
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QY 2101 CCTCCTACTACTAGTGTCTAGGAGCACTCTCCCGAGTCTTTGACAAACCAAAATATCTCT 2160
Db 1661 CCTCCTACTACTAAATACTTAAACAACTCCCCAATCTTAAACCAACCAAAATATCTCT 1602
QY 2161 AAACCTTGGCCACATGTCACCTAGTAGACAAACTCTCTGGTTAAGAGCTCGGGTTGAAAA 2220
Db 1601 AAACCTTTACACATATCACCTAAATAACAACTCCCTAATTAATAAATAAATAAATAA 1542
QY 2221 AATAACAAAGTAGTCTGGGAGTAGAGCCCAAGAGTAGGTAAATGGCTCAGAGAGGA 2280
Db 1541 AATAACAAATAATACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1482
QY 2281 GCCAAAAACAGGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATTTCTAGCAAGAGGTA 2340
Db 1481 ACCAAAAACAAATTTATACAAACGCTTAAACATATAATATAAATTTCTAACCAAAATA 1422
QY 2341 ACAGTGATCTGTCAGAGGCTTTTAAAGATTGCTGCTGCTGCTATGTGGAAGAGCAATG 2400
Db 1421 ACAATAATCTATCACAAACTTTTAAAAAATACTCTAACTACTATATAAAAAAATAA 1362
QY 2401 AAGGAGCAACAGTAAAAACAGGAGCCCGCAGGAGAGCTGTTACACAGTCCAGGCAAG 2460
Db 1361 AAAAAACACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1302
QY 2461 AGGTAGTGGAGTGGGCTGGGGAACAGAAAGAGGAGTGACAAACCACTGCTCTCTGAA 2520
Db 1301 AAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1242

QY	2521	TATATTCTGAAGGAGTTGCTCAAGGATTTCTATGTGTGAGAGAAAGAGAAATGG	2580	Db	162	ACCCAAACTATCATATAAAAAAACAACAACTACCACTCACCCTTCAAAAAATAAAA	103
Db	1241	TATATTCTAAAAAAATTTACTAAAAATTTCTATATATATATAAAAAAATAAAATAA	1182	QY	3661	CCAGACACAGCTCATGGTATGAGTTGATGCAGGTGTGGAGCCTCAACATCCTGCTCCC	3720
QY	2581	CTGGGTGTAGTAGTCATGCCAAGGAGGAGCGCAAGGAGACGATTTCCCTGAGCTCAGGA	2640	Db	102	CCAAACACAACTAATATATATAAATTAATACAAATATATAAAACCTCAACATCCTACTCCC	43
Db	1181	CTAAATATATAAATCACTACCAAAAAAATAACCAAAAAAACAATTCCTAAACTCAAAA	1122	QY	3721	CTCCTACTACACATGGTTAAGGCCTGTGTGCTGTGCTCTCCA	3760
QY	2641	GTTCAAGACCCAGCTCGGCAACACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	2700	Db	42	CTCCTACTACACATAAATAAAACCTATTACTCTCTATCTCCA	3
Db	1121	ATTCAAAACCAACCTTAACACACACACAAACAAACCCCTTCTCTACAAAAATACAAAAATTA	1062	RESULT 12			
QY	2701	GCTGGGTGTGGTGCACTGACCTGTGATCTCTAGCTACTCGGGAGCCTGAGGTGGAGGTA	2760	AAL36748			
Db	1061	ACTAAATATAATACATACACCTATAATCCTTAAGCTACTCGAAAACTAAAAATAAAAAATA	1002	XX	AAL36748 standard; DNA; 1712 BP.		
QY	2761	TTGCTTTGAGCCCGAGGAAGTTGAGGCTGCAGTCAGGCATGACTGTGCCACTGTACTTCAAC	2820	XX	AAL36748;		
Db	1001	TTACTTAAACCCCAAAAAATTAACACTACAATAAACCATAAATACCACTATACTTCAAC	942	XX	08-JAN-2002 (first entry)		
QY	2821	CTAGGTGACAGAGCAAGACCTGTCTCCCTGACCCCTGAAAAAGAGAAGAGTTAAAGT	2880	XX	Human musculoskeletal system related polynucleotide SEQ ID NO 3113.		
Db	941	CTAATAACAAACAAACCCCTTCTCCCTTAACCCCTTAACAAAAAATAAATAAAT	882	XX	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;		
QY	2881	TGACTTTGTCTTTATTTATTTATTTGCGCTGAGCAGTGGGTAATTTGGCAATGCCAT	2940	XX	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;		
Db	881	TAACTTTATCTTTATTTATTTTATTAACTTAACAATAAATAAATTAACAATACCAT	822	XX	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;		
QY	2941	TTCTGAGATGGTGAAGGCAGAGGAAGCAGTTTGGGGTAAATCAAGGATCTGCAATTTG	3000	XX	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;		
Db	821	TTCTAAATTAATAAACAACAAAAAATAAACAATTTAAATAAATCAAAAAATCTACATTT	761	XX	neurological disease; infection; human; secreted protein;		
QY	3001	GGACATGTTAAGTTTGAGATTCACGTGAGCTTCCAAAGTGTGAGGCCACATAGGCGATT	3060	XX	musculoskeletal system; ds.		
Db	762	AAACATTAATAAATTAATTCATCAACTTCCAAATATAAACCACATACACAATT	703	XX	Homo sapiens.		
QY	3061	CAGTGTGAAGATTCAGGACCAAGGTGGCAGGTGGCTCACTTCTGTAATCCAGCACT	3120	XX	WO200155367-A1.		
Db	702	CAATATAAATAATCAAAACCAAACTAAACACGATAAATCACTTCTATAATCCCAACACT	643	XX	02-AUG-2001.		
QY	3121	TTGGTGGCTGAGCGAGGTAGATCAATTTGAGTGCAGGAGTTTGAGACAAGCTTGGCCAACA	3180	XX	17-JAN-2001; 2001WO-US01338.		
Db	642	TTAATAAATCAAAACAAATAAATCAATTTAAATCAAAAAATTTAAACAAACACTTAACCAACA	583	XX	31-JAN-2000; 2000US-0179065.		
QY	3181	TGTTGAAACCCCATGTCTACTAAAAATACAAAAATAGCTGGTGGTGGCGCAGCCT	3240	XX	04-FEB-2000; 2000US-0180628.		
Db	582	TAAATAAACCCCATATCTACTAAAAATACAAAAATTAACCTAATATAAAGCAGCGCT	523	XX	24-FEB-2000; 2000US-0184664.		
QY	3241	ATAGTCCCAAGTTTTCAGAGGCTTAGGTAGGAGAAATCCCTTTGAACCCAGGAGGTGCAGG	3300	XX	02-MAR-2000; 2000US-0186350.		
Db	522	ATAATCCCAAAATTTTCAAAAACTTAAATAAAAAAATCCCTTAAACCCCAAAAAATACAAA	463	XX	16-MAR-2000; 2000US-0189874.		
QY	3301	TTGCAGTGAGCTGAGATTTGTCACCTGCACCTCCAGCCTGGGTGATGAGTGAGACTCTGT	3360	XX	17-MAR-2000; 2000US-0190076.		
Db	462	TTACAATAAACCAAAATTAATACCACTTACACTCCACCTTAAATATAAATAAATAAATCTAT	403	XX	18-APR-2000; 2000US-0198123.		
QY	3361	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	3420	XX	07-JUN-2000; 2000US-0209467.		
Db	402	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	343	XX	28-JUN-2000; 2000US-0214886.		
QY	3421	TCTAATTTGCCGTGACACCAACTCTCTGAGTTCACTAGCATGGCTAGACACACCTTAAC	3480	XX	30-JUN-2000; 2000US-0215135.		
Db	342	TCTAATTTACCCCTAAACACCAACTCTCTAATTTCACTAGCATTAACACACACCTTAAC	283	XX	07-JUL-2000; 2000US-0216847.		
QY	3481	ATTTTCTAGNATCCACCGCTTAGTGGAGTCTGCTAATCATGAGTATGGAATAGGT	3540	XX	11-JUL-2000; 2000US-0217487.		
Db	282	ATTTTCTAATAATCCCAACTTTAATAAATCTATCTAATCAATAAATAAATAAATAAAT	223	XX	14-JUL-2000; 2000US-0217496.		
QY	3541	CTGGGGCAGTGGGGTGGCAGCCAGCTGTGGCAGAGAAAGCAGACCAAGAAAGAGC	3600	XX	26-JUL-2000; 2000US-0220963.		
Db	222	CTAAACAAATAAAAAATAAACACCCAGTATAACAAAAAATAACACACAAAAAATAAC	163	XX	26-JUL-2000; 2000US-0220964.		
QY	3601	ACCCGAGCTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCCCTTCAAAAAATGAGGA	3660	XX	14-AUG-2000; 2000US-0224518.		

PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
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PR 14-SEP-2000; 2000US-0233063.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
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PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
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PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246529.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.

PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-451937/48.
XX
DR Isolated polypeptide for treating, preventing and/ or prognosing
XX disorders related to the musculoskeletal system including
XX musculoskeletal cancers and also for testing and detection e.g.
XX diagnosis -
XX
XX Example 2; SEQ ID NO 3113; 781pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
XX (ABR03087-ABR04109) associated with the musculoskeletal system useful
XX for preventing, treating or ameliorating medical conditions e.g. by
XX protein or gene therapy. The genes are isolated from a range of human
XX tissues disclosed in the specification. The nucleic acids, proteins,
XX antibodies and (ant)agonists are useful in the diagnosis, treatment
XX and prevention of: (a) cancer, e.g. breast and ovarian cancer and
XX other cancers of the adrenal gland, bone, bone marrow, breast,
XX gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
XX (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
XX healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
XX and (f) infectious diseases such as viral, bacterial, fungal and
XX parasitic infections.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1712 BP; 487 A; 361 C; 375 G; 489 T; 0 other;

Query Match 15.8%; Score 1712; DB 22; Length 1712;
Best Local Similarity 100.0%; Pred. No. 2.3e-291;
Matches 1712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8039 TACATGCATTACTGCATCCTTCTTACAATAATCTATGAGATAGGTACTATTATCCCC 8098
Db 1 tacatgcattactgccttcttacaataatctatgagataggtactattatcccc 60
QY 8099 ATTTCTTTTAAATGAAGAAGTAGCTAGCCGGCCGCTGGCTCACCCCTGTAATC 8158

Db	1141	caagtagctgggattacagcgctgcaccaccatgcgcccgcctgaatttttctgtatttttagta	1200
Qy	9239	GAGACAGGGTTTCCACCATGTTGGCCAGGTGCTCGAACTCTCCTGACCTCGTGTATCCG	9298
Db	1201	gagacaggggttccaccatgttgccagcggtgctcgcgaactctcctgacctgctgacccg	1260
Qy	9299	CTGCGCTCGGCCTCCAAAGTGTGAGATTACAGTGTGAGCCACCCTGCCAGCCGTCAC	9358
Db	1261	cctgcctcgccctcccaagtgctgagattacaggtgtagccacccctgcgcacgcgctca	1320
Qy	9359	AAAGAGTCTTAAATATATATATCCAGATGGCATGTGTTTACTTTATGTTTACTACATGC	9418
Db	1321	aagagcttcaatatataataccagatggcatgtgttactttatgttactacatgcact	1380
Qy	9419	TGGCTGCATAAATGTGGTACAAAGTCTGCTTTGAAGGCGCAGGTGCTTCAGGATACCA	9478
Db	1381	tggtgcataaattggtacaagcattctgtcttggaaggcaggtgctcgaagataccat	1440
Qy	9479	ATACAGCTCAGAAGTTCCTTTTAGGCATTAATAATTTAGCAAAAGATATCTCATCTCTT	9538
Db	1441	atacagctcagaagttctctcttagcattaaatttagcaagaatatactcatctcttc	1500
Qy	9539	TTTTAAACCATTTTCTTTTGTGGTTAGAAAGTTATGTAGAAAAAGTAAATGTGAT	9598
Db	1501	ttttaaacattttcttttttgggttagaaaaattatgtagaaaaaagtaaatgtat	1560
Qy	9599	TTACGCTCATGTGTAAGAAAGCTATAAATCAATACAAATTAAGCTGTATTTAATTTAG	9658
Db	1561	ttacgctcatgttagaaaagctataaaatgaatacaataaagctgttttaatttagcc	1620
Qy	9659	AGTGAAGAACTATTAAACAACTGTGCTATTACCTGTGTAGTATTATTGTGATTAATA	9718
Db	1621	agtgaaaaactattacaactgtctattaccctgttagtattattgttcattaaaaaag	1680
Qy	9719	CATATACTTTTAAATTAATGTATATTGTTATTTGTA	9750
Db	1681	catatactttaataaatgtattgtattgta	1712
RESULT 13			
ID	AAA96769	standard; cdna; 2506 BP.	
XX	AAA96769;		
XX	19-FEB-2001	(first entry)	
XX	cdna sequence encoding a histocompatibility iron loading (HFE) protein.		
XX	Human; histocompatibility iron loading protein; HFE protein;		
XX	major histocompatibility complex; non-classical class I gene;		
XX	chromosome 6p; iron disorder; haemochromatosis; ss.		
XX	Homo sapiens.		
XX	Key		
FH	Location/Qualifiers		
FT	1..1044		
FT	/*tag= a		
FT	/product= "histocompatibility iron loading (HFE) protein"		
FT	sig_peptide		
FT	1..66		
FT	/*tag= b		
FT	mutation		
FT	187		
FT	/*tag= c		
FT	/note= "if this base is mutated to G, then the		
FT	protein contains the mutation #63D"		
FT	193		
FT	/*tag= d		
FT	/note= "if this base is mutated to T, then the		
FT	protein contains the mutation #65C"		
FT	277		
FT	/*tag= e		
FT	/note= "if this base is mutated to C, then the		
FT	protein contains the mutation #93R"		

XX Busfield F, Cullen LM, Jazwinska EC, Powell LW;
PI WPI: 1998-179064/16.
XX Detection of autosomal recessive disorder - particularly hereditary
PT haemochromatosis, by detecting a mutation in the HC gene
XX Disclosure; Page -: 32pp; English.
XX This sequence represents the haemochromatosis (HC) gene. Mutations in
CC this sequence are detected using the method of the invention. The method
CC is for identifying an individual with hereditary haemochromatosis (HH) or
CC a predisposition to develop HH or to genetically pass on HH to an
CC offspring, comprising isolating a biological sample and amplifying a
CC region of genomic DNA in the biological sample encompassing all or part
CC of the DNA between markers D6S265 and D6S276, and detecting at least one
CC homozygous or heterozygous mutation in a nucleotide within the region.
CC The method can also be used for identifying an individual with an
CC autosomal recessive disorder (ARD) or predisposition to develop and/or
CC genetically pass on an ARD to an offspring, comprising isolating a
CC biological sample from the individual and screening genomic DNA in the
CC sample for the presence of a homozygous or heterozygous mutation in a
CC gene, the normal function of which, is required to prevent progression of
CC the disorder. The method(s) can be used to identify individuals that are
CC homozygous or heterozygous (carriers) for the mutation causing the ARD.
CC Especially the method is used to diagnose HH or predisposition to HH by
CC detecting a Cys282Tyr substitution. Individuals homozygous for this
CC mutation have HH and heterozygotes are potential carriers of the
CC disease.
XX Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;
SQ

Query Match 9.7%; Score 1051.6; DB 19; Length 2727;
Best Local Similarity 98.7%; Pred. No. 1.9e-175;
Matches 1060; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 7104 CAGGAGGCCGTCGCTACGCTTACGCTGAGTGAACGCTGAGTGAACGCTGAGCAG 7163
DB 1225 caagagagccatggggcactacgtcttagctgaacgtgagtgacacgcagcctgcagac 1284
QY 7164 TCACCTGTGGGAGGAGACAAACTAGAGACTCAAGAGGGAGTGCATTTATGAGCTCTTC 7223
DB 1285 tcaactgtgggaagagacaaactagagactcaagagggagtgacattatgagctcttc 1344
QY 7224 ATGTTTCAGGAGAGAGTTGAACCTTAACATAGAAATTCCTGAGCAACTCCTTGATTTTA 7283
DB 1345 atgtttcagagagagagttgaacctaaacatagaaattgcctgacgaactccttgattta 1404
QY 7284 GCCTTCTCTGTTCATTTCTCAAAAAGATTTCCCATTTAGGTTTCTGAGTCTCTGCATG 7343
DB 1405 gctctctctgttcattctcctcaaaaagattccccattagggttctgagttcctgcag 1464
QY 7344 CCGGTGATCCCTGAGCTGTGACCTTCGCCCTGGAACTGTCTCTCATGAACCTCAAGCTGCA 7403
DB 1465 ccggtgatccctagctgtgacctctcccctggaaactgctctcatgaaacctcaagctgca 1524
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DB 1525 tctagaggtctcttcattctcctcgtcacctcagagacacacacctatgctcattcatt 1584
QY 7464 TCCTATTTTGGAGAGGAGCTCTTTAAATTTGGGGGACTTACATGATTCATTTTAAACATC 7523
DB 1585 tctatttttggagaggagactcctaaatttgggggacttacatgattcattttaacatc 1644
QY 7524 TGNAAAAAGCTTTGAACCTGGGAGCTGGCTAGTACATACACCTTACCAGATTTTACACAT 7583
DB 1645 tdagaaaagctttgaaacctggagcgtgctagtcataaacctaccagattttttacacat 1704
QY 7584 GTATCTATCATTTTCTGGACCCGPTCAACTTTTCCCTTTGAATCCTCTCTCTGTGTTACC 7643
DB 1705 gtatctatgcatcttctggacccttcaacttttccctttgaaatcctctctctgtgttacc 1764

QY 7644 CAGTAACCTCATCTCTCACCAGCCTTGGGATCTTCCATCTGATTTGTGATGTGAGTTGC 7703
DB 1765 cagtaacctcatctctcaccagccttgggattcttccatctctgattgtgatgagtgctgc 1824
QY 7704 ACAGCTATGAAGGCTGTACACTGCACGAATGAAGAGGACCTGTGCCAGAAAAAGCATC 7763
DB 1825 acagctatgaaggctgtgactgcacgaatggaagagggcactgtcccagaaaaagcatc 1884
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DB 1885 atggctatctctgggttagtatgaggtgttttttagcaggtaggagcacaatatctctgaa 1944
QY 7824 AGGGCTTCTGAAGAGGCTGTTTTTCTTAATGGCATGAAGGTGTCATACAGATTTGCAAA 7883
DB 1945 aggggtgtggaagagggtgttttttctaattggcatgaaggtgcatacagatttgcaga 2004
QY 7884 TTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTATTCAGACCTGGAAGATCACAA 7943
DB 2005 tttaatggctcttcttgggatgctactctagtattccagacctgaagaatcacata 2064
QY 7944 ATTTCTACCTGGTCTCTCTCTTGTCTGATAAATAATATGATAAGGATGATAAAGC 8003
DB 2065 attttctactcgtctctcctgttctgataatgaaattatgataagatgataaagc 2124
QY 8004 ACTTACTTCTGTCGACCTCTTCTGAGCAGCTACTTACATGCAATTTACTGCATGCACTTCT 8063
DB 2125 acttactcgtgtcgcactcttctgagcactactacattacattcattcattcattcatt 2184
QY 8064 TACAATAATTTCTATGATAGTACTATTTATCCCATTTCTTTTAAATGAAGAAAGTG 8123
DB 2185 tacaataattctatgagataggtaactattatccccattctctttttaaataagaagaagt 2244
QY 8124 AAGTAGGCCGGCAGCGGTGCTCAGCGCTGTAAATCCAGACCTTTGGGAGGCCA 8177
DB 2245 aagtaggcggggcaggtggctgcgcctgtgtcccgagggtgctgagattgca 2298
RESULT 15
AAC68440
ID AAC68440 standard; DNA; 517 BP.
XX AAC68440;
XX 21-FEB-2001 (first entry)
XX Human hereditary hemochromatosis DNA used for mutation detection.
DE HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ss.
XX Homo sapiens.
XX US6140305-A.
XX 31-OCT-2000.
XX 04-APR-1997; 97US-0834497.
XX 04-APR-1996; 96US-0630912.
XX 16-APR-1996; 96US-0632673.
XX 23-MAY-1996; 96US-0652265.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX WPI: 2001-006341/01.
XX New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -

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XX      Disclosure; Fig 6; 108pp; English.
PS
XX
XX      The present invention relates to hereditary hemochromatosis gene
CC      products. These proteins may be used to treat a patient diagnosed as
CC      having human hemochromatosis disease. It is also useful as a metal
CC      chelation agent or as a T-cell differentiation factor, and for
CC      alleviating iron overload. They may also be used in protein replacement
CC      therapy for individuals having a defective human hemochromatosis gene.
XX
SQ      Sequence 517 BP; 126 A; 120 C; 147 G; 124 T; 0 Other;

      Query Match          4.8%; Score 516; DB 22; Length 517;
      Best Local Similarity 99.8%; Pred. No. 1.5e-81;
      Matches 516; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5507 TATTTCTCTCCCTCCAAACCTATAGAGGAGTGAAAGTTCCAGTCTTCTGTGCAAGGGTAA 5566
Db      1 tatttcttctccaaacctatagaaggaagtgaaagtccaggttccagttcttccctggcaagggtaa 60

Qy 5567 ACAGATCCCTCTTCCTCATCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 5626
Db      61 acagatccctctctctctctctctctctctctctctctctctctctctctctctctctctct 120

Qy 5627 CACATCATGTGACCTCTTCAGTGCACCACTCTACGGTGTGGGGCTTGAACTACTACCCCC 5686
Db      121 cacatcatgtgacctctctcagtgaccacctctacggtgtcgggccttgaaactactaccccc 180

Qy 5687 AGACATCACCATGAGTGGCTGAAGGATAGCAGCCCAATGGNTGCCAAGAGTTCCGAC 5746
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Qy 5747 CTAAGACGTATTGCCCAATGGGGATGGGACCTACAGGGTGGGATAACCTTGGCTGTAC 5806
Db      241 ctaagacgtatlgcccaatgggatgggacccctaccagggtgataaaccttggctgtac 300

Qy 5807 CCCCTGGGGAAGACGAGATATACGTNCCAGGTGGAGCACCCAGGCCCTGGATCAGCCCC 5866
Db      301 cccctggggaagacgagatatacagtgccaggtggagcaccacccaggcctggatcagcccc 360

Qy 5867 TCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGG 5926
Db      361 tcattgtgactggggtatgtgactgatgagagccagagctgagaaaaatctattggggg 420

Qy 5927 TTGAGAGGAGTGCCTGAGGAGGTAAATTATGCGAGTGAGATGAGGATCTGCTCTTTGTTAG 5986
Db      421 ttgagaggagtgcctgagagggtaatatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 480

Qy 5987 GGGGTGGGCTGAGGGTGGCAATCAAGGCTTTAACTT 6023
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Search completed: June 19, 2002, 17:56:01
 Job time: 12448 sec

OY 8847 AGTGCCTTGAGTACAGAACTCTGGTGTATTTCCCTCAATGAAGTGAAGTCTCT 8906
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 Db 345 AGTCCCTCTGGAGTCAGAACTCTGTGTATTTCCCTCAATGAAGTGAAGTCTCT 286
 OY 8907 CATTTTGAGTGTATATGGAAGCCACCAAGTGGCTTAAGAGTGGCCAGTCTTCCA 8966
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 OY 8967 TGGAG-CCACTGGGGTTCGGGTGCACATTTAAAAAAAATCTAACAGGACATTCAGAA 9025
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 Db 225 TGGAGCCCATTTGGGGTTCGGGTGCACATTTAAAAAAAATCTAACAGGACATTCAGAA 166
 OY 9026 TTGCTAGATTTGGGAAATCAGTTCACCAGTTCACAAAGAGTC-TTTTTTTTTTTTTTGA 9084
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 Db 165 TTGCTAGATTTGGGAAATCAGTTCACCAGTTCACAAAGAGTCTTTTTTTTTTTTTTGA 106
 OY 9085 GACCTATTTGCCAGGCTG 9103
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 Db 105 GACCTATTTGCCAGGCTG 87

RESULT 13
 LOCUS A0111002 443 bp DNA linear GSS 29-AUG-1998
 DEFINITION CIT-HSP-2370L14.TR CIT-HSP Homo sapiens genomic clone 2370L14, DNA
 sequence.
 ACCESSION A0111002
 VERSION A0111002.1 GI:3487692
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 443)
 Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
 Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
 Venter,J.C.
 Title
 Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building
 Unpublished (1998)
 Other GSS: CIT-HSP-2370L14.TF
 JOURNAL
 COMMENT
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mhadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

TITLE
 Map Building
 Unpublished (1998)
 Other GSS: CIT-HSP-2370L14.TF
 JOURNAL
 COMMENT
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mhadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES
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Query Match 3.8%; Score 408.4; DB 12; Length 443;
 Best Local Similarity 99.5%; Pred. No. 9.3e-48;
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 OY 2752 TGGAGGATTTGCTTGAGCCCAAGAAATTGAGGCTGAGTGAAGCCATGACTGCGCACTG 2811
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Db 443 TGAAGGATATTCCTTGAGCCCAAGAAATTGAGGCTGCACTGAGCCATGACTGCGCACTG 384
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 Db 383 TACTTACGCTAGTGTACAGACAGACCTGTCCTCCCTGACCCCTGAAAGAGAA 324
 OY 2872 AGTTAAAGTTGACTTTGTTCTTTATTTTAAATTTTATTTGAGCAGTGGGTAATGG 2931
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 Db 323 AGTTAAAGTTGACTTTGTTCTTTATTTTAAATTTTATTTGAGCAGTGGGTAATGG 264
 OY 2932 CAATGCATTTTCTGAGATGTGTAGAGCAGAGAAAGACGATTTGGGGTAAATCAAGAT 2991
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 Db 263 CAATGCATTTTCTGAGATGTGTAGAGCAGAGAAAGACGATTTGGGGTAAATCAAGAT 204
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 Db 144 TAGCAGTTCACTGTAAAGATTCAGAGCCAGGCTGGGCGGCTCACTTCTGTAT 85
 OY 3112 CCCAGCACTTTGGTGGCTGAGCAGGATGATCATTTGAGCTGAGAGATTGAGACAGCT 3171
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 OY 3172 TG 3173
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 Db 24 TG 23

RESULT 14
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 mRNA sequence.
 ACCESSION AA569989
 VERSION AA569989.1 GI:2343969
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 453)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cdNA Library Preparation: M. Bento Soares, Ph.D.
 cdNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html
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 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 428.

FEATURES
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 /tissue_type="breast"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cdna was prepared from pooled bulk
 breast tumor tissue, and was then primed with a Not I -

[illegible]

QY	3165	ACNAGCTT	3172
Dd	54	ACATGCTT	47
RESULT_12			
LOCUS	AM299376/c	525 bp	mRNA
DEFINITION	xsa39b06.x1 NCI.GCAP_Kid1 Homo sapiens cDNA IMAGE:271987 3'	linear	EST 18-JAN-2000
ACCESION	AM299376		
VERSION	AM299376.1		
KEYWORDS	similar to contans element MER37 repetitive element ; , mRNA sequence.		
SOURCE	EST.		
ORGANISM	Homo sapiens human. <i>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</i>		
REFERENCE	Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgapbs@renal.nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E Consortium/LNL at: www.bio.lnl.gov/bdrp/image/Image.html Seq primer: -40UP from Gibco High quality sequence stoppers 464.		
FEATURES	location/Qualifiers		
source	1..525 <code>/organism="Homo saplens"</code> <code>/db_xref="taxon:9606"</code> <code>/clone="IMAGE:271987"</code> <code>/clone_idb="NCI_GCAP_Kid11"</code> <code>/lab_host="DHIOB"</code> note="Organ: kidney; Vector: pTZ19-D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA from the normalized library NCI.CGAP.Kids was prepared, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cdnas from a pool of 5,000 clones made from the same library (clones IDs 1322376-1323911, 1456007-1456775, and 1500532-1502853). Subtraction by Bento Soares and M. Fatima Bonaudo."		
BASE COUNT	153 A 123 C 125 G 124 T		
ORIGIN			
Query Match	3.8%; Score 411.8; DB 9; Length 525;		
Best Local Similarity	99.1% Pred. NO. 2.g-e-48;		
Matches	435; Conservative 0; Mismatches 2; Indels 2; Gaps 2;		
QY	8667	CAGATCCAGGTGCATCATTTTCATTAAAGCCTTGGAAGAAGGTCTGGATGTGAC	8726
Dd	525	GTAATCCATAAGTCAITCTTCCTTTAAAATGCCCTGAAGSAAGSTCTGGAATGTGAC	466
QY	8727	TCCCTGTACTCTGTGTGCTCTTTTGACATTTCTTTTGACCTAACGACAAGACTG	8786
Dd	465	FCCCTGTCTCTGTGTGCTCTTTTGACATTTCTTTTGACCTAAGCAAAGACTG	406
QY	8787	TAATTGTGGGACACACTAGTAGTGGCCCTGCTGGGCTTCACACAGSGTGTCTCCCAGGCC	8846
Dd	405	TAATTGTGGGACACACTAGTAGTGGCCCTGCTGGGCTTCACACAGSGTGTCTCCCAGGCC	346

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Db 404 CCAGCCGCAAAAGAGCTTAATATATATCCAGATGCGATGCTTACTTATGTTAC 345
Oy 9499 TACATGCACTGGCGCATTAATGTCGTACAGACATTCCTGCTGAAGGCGAGTGCTTC 9468
Db 344 TACATGCACTGGCGCATTAATGTCGTACAGACATTCCTGCTGAAGGCGAGTGCTTC 285
Oy 9469 AGATACCATATACAGCTCAGAGAGTTCTCTTAGCGCATTAATTTTACCAAGATATC 9528
Db 284 AGATACCATATACAGCTCAGAGAGTTCTCTTAGCGCATTAATTTTACCAAGATATC 225
Oy 9529 TCATCTCTCTTTTAAACCAATTTCTTTTGTGCTAGAAAAGTATATGAAAAAG 9568
Db 224 TCATCTCTCTTTTAAACCAATTTCTTTTGTGCTAGAAAAGTATATGAAAAAG 165
Oy 9589 TAAATGATTTAGCGCTATGTAGAAAAGTATTAATGATTAAGCTGTTAT 9648
Db 164 TAAATGATTTAGCGCTATGTAGAAAAGTATTAATGATTAAGCTGTTAT 105
Oy 9649 TTAATTAAGCAAGTGAACCTATTAACCACTGCTATTAACCTGTTATTTGTTGC 9708
Db 104 TTAATTAAGCAAGTGAACCTATTAACCACTGCTATTAACCTGTTATTTGTTGC -C 46
Oy 9709 ATTAAAAATGCATATCTTTTAAATTAAGTATTTGTTATTA 9752
Db 45 ATTAAAAATGCATATCTTTTAAATTAAGTATTTGTTATTA 2

RESULT 10
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LOCUS UI-H-B13-akv-c-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone
DEFINITION IMAGE:2735605 3', mRNA sequence.
ACCESSION AM449998
VERSION AM449998.1 GI:6990774
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I M A G E Consortium/ILIN: at:
www-bio.liln.gov/bdrip/image/image.html
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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/lab_host="NCI_CGAP_Sub5"
/note="Vector: pT73D-Pac (Pharmacia)"
polylinker: Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub5
is a subcloned library derived from NCI_CGAP_Sub4. The
NCI_CGAP_Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI_CGAP_kids pool 1 LHAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids
13223/6-1323/11, 1456008-1456775, 1500552-1502855));
NCI_CGAP_kids pool 1 LHAM 3338-3342, 3722-3725, 3776-3778

(IMAGE Clonoids 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI_CGAP_Lus pool 1 LHAM 3575-3582,
3851-3854 (IMAGE Clonoids 1414920-1417991, 1520004-1522439
); NCI_CGAP_Gc4 pool 1 LHAM 3164-3167, 3716-3720,
3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI_CGAP_Px2 pool 1 LHAM 2457-2459,
2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759
), 1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1
LHAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255
), 1144584-1145351). (10% of the driver population), plus a
pool of 3,840 arrayed clones from NCI_CGAP_Sud1 (IMAGE
Clonoids 2708616-2710535) and NCI_CGAP_Sud2 (IMAGE
Clonoids 2710536-2712455) (10% of the driver population
), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE
Clonoids 2712456-2723591) (10% of the driver population),
plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE
Clonoids 2723592-2728969) (70% of the driver population).
Subtraction was performed as previously described (Bonaldi
, Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806.
TAG_LIB=NCI_CGAP_Co10
TAG_TISSUE=colon
TAG_SEO=AAACG"

BASE COUNT 93 a 125 c 134 g 90 t
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Best Local Similarity 99.5%; Pred. No. 1.7e-49;
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 325 GATATTAAAGGGGAGCGCGGCAAGCTGGGGAATATGGCCCGGAGCCAGCGCGG 384
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Oy 385 CTTCCTCCTCGATGCTTTTGCAGACCGGCGCTGACGGGCGCTGCTGCTGATCC 444
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Oy 445 GAGGCGTGGGCGGCACTGAGGGGCGGGGCTGGAATAATCGAACTAGCTTTTCT 504
Db 320 GAGGCGTGGGCGGCACTGAGGGGCGGGGCTGGAATAATCGAACTAGCTTTTCT 261
Oy 505 TTGCGCTGGGAGTTTGCTAACTTTGAGAGACCTGCTCAACCTATCCGCAAGCCCTCT 564
Db 260 TTGCGCTGGGAGTTTGCTAACTTTGAGAGACCTGCTCAACCTATCCGCAAGCCCTCT 201
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Db 140 TCCTGCGCCAGAGCTGCCCCCTGCTCCCGGCTGTCGGGCTGCGGAGTGACTTTTG 81
Oy 685 GAAACCGCCACCTCCCTTCCCGCACTAGAAATGCTTTAAATAATGCTAGTCTCTC 744
Db 80 GAAACCGCCACCTCCCTTCCCGCACTAGAAATGCTTTAAATAATGCTAGTCTCTC 21
Oy 745 TTGA 748
Db 20 TTGA 17

RESULT 11
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DEFINITION HS-2239.B1.D04_MR_CTR Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-2239 Col-7 Row-H, DNA sequence.
ACCESSION A0790990
VERSION A0790990.1 GI:5698614
KEYWORDS GSS.

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 520) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdnp/image/image.html Seq primer: -400P from Glbco High quality sequence stop: 406. Location/Qualifiers
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BASE COUNT	171 a 84 c 82 g 183 t
ORIGIN	
Query Match 3.9%; Score 423.4; DB 9; Length 520; Best Local Similarity 97.5%; Pred. NO. 6.9e-50; Matches 430; Conservative 0; Mismatches 11; Indels 0; Gaps 0;	
9312 CCCAAGTCCTAGATTACAGGTGAGCGACCCGCGCCAGCGCTCAAT 9371 463 CCCAGGCTCTGAGTTCAGGCTGAGCCACCCCTCCAGCGCTCAAT 404 9372 ATATATATCCAGATGGCATGTGTTACTTATGTTACTACATGCACTGGTGATTAAT 9431 DB 403 ATATATATCCAGATGGCATGTGTTACTTATGTTACTACATGCACTGGTGATTAAT 944 9432 GGTGTCAAGCATCTGCTTGAAGGGGAGGCTTCAGAGTACATATACAGCTAGAA 9491 DB 343 GTGTGTCAGCATCTGCTTGAAGGGGAGGCTTCAGAGTACATATACAGCTAGAA 284 9492 GTTCTCTCTTAGCATTAATTTTGAAGCAAGATATCTCATCTCTCTTTTAAACATTT 9551 DB 283 GTTCTCTCTTAGCATTAATTTTGAAGCAAGATATCTCATCTCTCTTTTAAACATTT 224 9552 TCTTTTGTGTGTTGAAGAAAGTTATGTGAAAAAGTAAATGTAATTTAGCGTCAATTG 9611 DB 223 TCTTTTGTGTGTTGAAGAAAGTTATGTGAAAAAGTAAATGTAATTTAGCGTCAATTG 164 9612 AGAAAAGCTTAAATGAATACAAATTAAGCTGTATTTAATTAGCCAGTGAAGAACTAT 9671 DB 163 AGAAAAGCTTAAATGAATACAAATTAAGCTGTATTTAATTAGCCAGTGAAGAACTAT 104 9672 TAACAACCTGTGATTAACCGCTTAGATTAATGTGTGATTAAGAAATGATATCTTAAT 9731 DB 103 TAACAACCTGTGATTAACCGCTTAGATTAATGTGTGATTAAGAAATGATATCTTAAT 44	

[illegible]

prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 153 a 77 c 68 g 141 t 1 others
ORIGIN

Query Match 4.08; Score 429.4; DB 9; Length 440;
Best Local Similarity 98.4%; Pred. No. 1.1e-50;
Matches 433; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 9313 CCAAGTGTGAGATTCAGGTGAGCCACCGCCAGCCGTCMAAGAGCTTAAATA 9372
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DB 440 CCAGGCTGCTGAGATGAGGTGAGCCACCGCCAGCCGTCMAAGAGCTTAAATA 381
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DB 380 TATATATCCAGATGGCATGTGTACTTATTTACTACATGCACTGGCTGCATAATG 321
QY 9433 TGGTCAAGCATTCCTGCTTGAAGGAGGCTGCTCAGATACATATACACTAGAG 9492
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DB 320 TGGTCAAGCATTCCTGCTTGAAGGAGGCTGCTCAGATACATATACACTAGAG 261
QY 9493 TTTCTCTTTAGCATTAATTTTACGAAGATATCTCATCTCTTTTAAACATTTT 9552
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QY 9553 CTTTCTTTAGCATTAATTTTACGAAGATATCTCATCTCTTTTAAACATTTT 9612
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QY 9613 CAAAGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 9672
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DB 80 AACACTGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 21
QY 9733 AATGATATTTGATTTATA 9752
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DB 20 AATGATATTTGATTTATA 1

RESULT 7
AAB76054/c 439 bp mRNA linear EST 31-MAR-1998
LOCUS nrl4d03.s1 NCI_CGAP_Col0 Homo sapiens cDNA clone IMAGE:116197 3'
DEFINITION similar to contains element MER36 repetitive element ; mRNA
sequence.
ACCESSION AAB76054
VERSION AAB76054.1 GI:2984817
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 439)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Ilian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.ljll.gov/bdnp/image/image.html
Insert Length: 865 Std Error: 0.00
Seq primer: -40m13 fwd, 5' from Amersham
High quality sequence stop: 421.
location/Qualifiers

FEATURES
source

1. .439
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1161797"
/clone_lib="NCI_CGAP_Col0"
/tissue_type="colon tumor RER+"
/lab_host="DH108"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."
BASE COUNT 154 a 77 c 66 g 142 t
ORIGIN

Query Match 3.98; Score 427; DB 9; Length 439;
Best Local Similarity 98.9%; Pred. No. 2.3e-50;
Matches 430; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9318 GTGCTGAGATTCACAGTGTGAGCCACCGCCAGCCGTCMAAGAGCTTAAATATAT 9377
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 439 GTGCTGAGATTCACAGTGTGAGCCACCGCCAGCCGTCMAAGAGCTTAAATATAT 380
QY 9378 ATCCAGATGGCATGTGTACTTATTTACTACATGCACTGGCTGCATAATGATG 9437
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 379 ATCCAGATGGCATGTGTACTTATTTACTACATGCACTGGCTGCATAATGATG 320
QY 9438 CAAGCATTCCTGCTTGAAGGAGGCTGCTCAGATACATATACAGCTCAGAACTTCT 9497
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 319 CAAGCATTCCTGCTTGAAGGAGGCTGCTCAGATACATATACAGCTCAGAACTTCT 260
QY 9498 TCTTTAGCATTAATTTTACGAAGATATCTCATCTCTTTTAAACATTTTCTTT 9557
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 259 TCTTTAGCATTAATTTTACGAAGATATCTCATCTCTTTTAAACATTTTCTTT 200
QY 9558 TTTGTGCTTGAAGGAGGCTGCTCAGATACATATACAGCTCAGAACTTCT 9617
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 199 TTTGTGCTTGAAGGAGGCTGCTCAGATACATATACAGCTCAGAACTTCT 140
QY 9618 GCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 9677
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 139 GCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 80
QY 9678 CTTGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 9737
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 79 CTTGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 20
QY 9738 AATGATATTTGATTTATA 9752
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 19 AATGATATTTGATTTATA 5

RESULT 8
A1949947/c 520 bp mRNA linear EST 06-SEP-1999
LOCUS wq04f05.x1 NCI_CGAP_K1012 Homo sapiens cDNA clone IMAGE:2470305 3'
DEFINITION mRNA sequence.
ACCESSION A1949947
VERSION A1949947.1 GI:5742257
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens

OY	4388	GGAATTTCAGAGGTGGTGCCTGAGCGTGCCATCCTGCCAAATTTGGAGAAGGACCTTTCTCA		4647
Dd	282	GGAGTTTCAGAGGTGGCTGAGCGTGCCATCCTGCCAAATTTGGAGAAGGACCTTTCTCA		341
OY	4648	ATTCCTGAGACTCTCTACCCTTAATAATGAGANTSTATGAGACAAGCACAAATCATGGTTTTAA		4707
Dd	342	ATTCCTGAGACTCTCTACCCTTAATAATGAGANTSTATGAGACAAGCACAAATCATGGTTTTAA		401
OY	4708	TTCCTTTTCCATGATGATATGGCTCAAAGGAGAACGTCTAATGGCCCCCTGGCTTTTAATTA		4767
Dd	402	TTCCTTTTCCATGATGATATGGCTCAAAGGAGAACGTCTAATGGCCCCCTGGCTTTTAATTA		461
OY	4768	ACCAATTAATCTTTTGTATATTTATACCTGTTAAAATTCAGAAATGTCAGAGCCGGGCAC		4827
Dd	462	ACCAATTAATCTTTTGTATATTTATACCTGTTAAAATTCAGAAATGTCAGAGCCGGGCAC		521
OY	4828	GGTAGGCCTCA	4836	
Dd	522	GGTAGGCCTCA	530	
RESULT	5	AII27651	438 bp	MRNA linear EST 27-OCT-1998
LOCUS	AII27651/c	gc30n07.xl Soares pregnant uterus NBHpu Homo sapiens cDNA clone IMAGE:1711165_3' similar to contains element MER36 repetitive element ; mRNA sequence.		
DEFINITION		AII27651		
VERSION	AII2765L.1	GI:3596165		
KEYWORDS	EST.			
SOURCE ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
JOURNAL TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov This clone is available royalty-free through LNLN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 669 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amershams High quality sequence stop: 415. Location/Qualifiers 1..438 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1711165" /cloned_lib="Soares_pregnant_uterus_NBHPU"			
FEATURES	source	/sex="female" /dev_stage="adult" /lab_host="DHIOB" note="Organ: uterus; Vector: pVT73-Pac; site_1: Not I; site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGAGAGATTCGCGCGCCCTTTTCTTTTCTTTTCTTTT 3']". double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pVT73 vector Library went through one round of normalization. Library constructed by M. Fatima Boudalou."		
BASE COUNT	153 a	73 C	67 g	145 t
ORIGIN				

FEATURES	source
Db 9317	AGCTGAGATTACAGGGGTGGAGCCACCCGACCGCCAGCCGCAAAAAGAGCTTAAGATATA 9376
Oy 9317	AGCTGAGATTACAGGGGTGGAGCCACCCGACCGCCAGCCGCAAAAAGAGCTTAAGATATA 9376
Db 438	AGTGTGAGATTACAGGGGTGGAGCCACCCGACCGCCAGCCGCAAAAAGAGCTTAAGATATA 379
Oy 9377	TATCCAGATGCGATGTGTTTACTTTATGTATGTAACATGACACTTGGCTCATTAATGTGGT 9436
Db 378	TATCCAGATGCGATGTGTTTACTTTATGTATGTAACATGACACTTGGCTCATTAATGTGGT 319
Oy 9437	ACAAGCATTCGTGCTTGAAGGGCAGCTGCTTCAGATACATATACAGCGCAAGAGTTTC 9496
Db 318	ACAAGCATTCGTGCTTGAAGGGCAGCTGCTTCAGATACATATACAGCTCAGAAAGTTTC 259
Oy 9497	TTCTTTAGGCATTAAATTTTATAGCAAGATATCATCTCTCTTTTAAACCATTTTCCTT 9556
Db 258	TTCTTTAGGCATTAAATTTTATAGCAAGATATCATCTCTCTTTTAAACCATTTTCCTT 199
Oy 9557	TTTTGTGCTAGAAAAGTTATGTACAAAAAAGTAAATGTTGTTTACGCATCATGTGAGAA 9616
Db 198	TTTTGTGCTAGAAAAGTTATGTACAAAAAAGTAAATGTTTACGCATCATGTGAGAA 139
Oy 9617	AGCTATAAATGAAATACAAATTAAGCTGTATTTTAATTTAGCCAGTGAAACATATTACA 9676
Db 138	AGCTATAAATGAAATACAAATTAAGCTGTATTTTAATTTAGCCAGTGAAACATATTACA 79
Oy 9677	ACTGTGTAATACCTGTATGTATTTATGTGTGCATTAATAAATGATATCTTATTAATAG 9736
Db 78	ACTGTGTAATACCTGTATGTATTTATGTGTGCATTAATAAATGATATCTTATTAATAG 19
Oy 9737	TATATTTGATTTGATA 9752
Db 18	TACATTTGATTTGATA 3
RESULT 6	
LOCUS	AM469921 440 bp mRNA linear EST 24-FEB-2000
DEFINITION	ha27E08.X1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874950 3'
ACCESSION	AM469921
VERSION	AM469921.1 GI:7040027
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 440)
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www-bio.lnl.nh.gov/bhpr/image/image.html Seq primer: -40UP from Gibco High quality sequence stop: 439. Location/Qualifiers 1..440

Query Match	4.08;	Score 429.6;	DB 9;	Length 438;
Best Local Similarity	99.18;	Pred. No. 1e-50;		
Matches 432;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

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/lab_host="Dh10B"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
plasmid DNA from the normalized library NCl_CGAP_Kids was

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DEFINITION	EST836265 MAGE resequences, MAGM Homo sapiens CDNA, mRNA sequence
ACCESSION	AM974162
VERSION	AM974162.1 GI:8165353
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 545) Hedge, P., Qi, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johng@tigr.org Plate: 330
FEATURES	Seq. primer: Forward
source	Location/Qualifiers 1..545 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MAGE resequences, MAGM" /note="Vector: pBluescriptSKm"
BASE COUNT	153 a 137 c 123 g 132 t
ORIGIN	
Query Match	4.3%; Score 464.8; DB 9; Length 545;
Best Local Similarity	93.8%; Pred. No. 1.1e-55;
Matches	484; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY	8576 GAAAGAGAGAGANTGGCTCTCTCTGTGCATATGTGTCTCTCTGAGAGCTTGAAT 8635
DB	544 GAAAGGGGGTGCGTCTTTTCTTCTGTCCAAAGGGTTTCTTTAAGGAGCTTGAAT 485
QY	8636 CACATGAGGGGAAAGCAAGAAACAAACCACTGATCTCTAGCTGTGCATGTTTCCTTTA 8695
DB	484 CCAAGAGAGGGGACACAGAAACAAACCACTGTCTCCAAAGGGTATGTTCCTTTTA 425
QY	8696 AAGTCCCTGAAGAGAGTCTCTGGAATGTGACTCCCTTGCCTCTGTGTCTCTTTGGG 8755
DB	424 AAGTCCCTGAAGAGAGTCTCTGGAATGTGACTCCCTTGCCTCTGTGTCTCTTTGGG 365
QY	8756 ATTCAATTCTTGTGGACCTTACGCAAGAGACTGAATTTGGTGGGACAGCTAGTGCCCTCG 8815
DB	364 ATTCAATTCTTGTGGACCTTACGCAAGAGACTGAATTTGGTGGGACAGCTAGTGCCCTCG 305
QY	8816 TGGGCTTACACACGGGTGTCTCTCTAGGCCAGTGTCTGTGAGTCAAACTGTGGT 8875
DB	304 TGGGCTTACACACGGGTGTCTCTCTAGGCCAGTGTCTGTGAGTCAAACTGTGGT 245
QY	8876 ATTTCCTCATGTAATGAGTAACTGTCTCATATTTGAGATGATATATGAAGACACC 8935
DB	244 ATTTCCTCATGTAATGAGTAACTGTCTCATATTTGAGATGATATATGAAGACACC 185
QY	8936 AAGTGGCTTAGAGAGATGCCAGAGTCTCTCATGAGACCACTGGGGTTCCGGTGCACATTA 8995
DB	184 AAGTGGCTTAGAGAGATGCCAGAGTCTCTCATGAGACCACTGGGGTTCCGGTGCACATTA 125
QY	8996 AAAAAAAAAATCTAACCCAGACATTTAGGAATTTGATAGATTTGTGGAAATAGTTTCAACAT 9055
DB	124 AAAAAAAAAATCTAACCCAGACATTTAGGAATTTGATAGATTTGTGGAAATAGTTTCAACAT 65
QY	9056 GTTCAAAAGAGTCTTTTTTTTTTTTTTTTGTAGACTCA 9091
DB	64 GTTCAAAAGAGTCTTTTTTTTTTTTTTTTGTAGACTCA 29

RESULT	4	531 bp	DNA	linear	GSS	07-JUL-1999
LOCUS	AO703007					
DEFINITION	HS_5443.B1.G09_17A RPl-11 Human Male BAC Library Homo sapiens genomic clone Plate-1019 Col-17 Row-N, DNA sequence.					
ACCESSION	AO703007					
VERSION	AO703007.1	GI:5412433				
KEYWORDS	GSS.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo. 1 (bases 1 to 531)					
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,D., Zhao,S., Adams,M.D. and Koller,L.					
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome					
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)					
MEDLINE	99380589					
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPl-11. For BAC library availability, please contact Plier de Jong (plierdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.husc.washington.edu Plate: 1019 row: N column: 17 Seq primer: 17 Class: BAC ends High quality sequence stop: 531.					
FEATURES	Location/Qualifiers					
SOURCE	1..531					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/clone_plate="1019 Col-17 Row-N"					
	/clone_lib="RPl-11 Human Male BAC Library"					
	/sex="male"					
	/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"					
BASE COUNT	129 a 114 c 146 g 137 t	5 others				
ORIGIN						
Query Match	4.3%	Score 464.2	DB 12	Length 531		
Best Local Similarity	96.5%	Pred. No. 1.3e-55				
Matches 472	Conservative 0	Mismatches 17	Indels 0	Gaps 0		
4348	ACACTGATTGGAGACACAGAACCCAGGGCTGGGCCACCAAGCTGGAGTGGAAAGC	4407				
Db	42	ACACTGATTGGAGAGACAGACAGAACCCAGGGCTGGGCCACCAAGCTGGAGTGGAAAGC	101			
Oy	4408	CACAAAGTTGGGGCCAGGCGAAGACGGGCTTAATCTGGAGAGGAGCTGCCCTGCACAGCTG	4467			
Db	102	CTCTGTGATTTGGGGCCAGGCGAAGACGGGCTTAATCTGGAGAGGAGCTGCCCTGCACAGCTG	161			
4468	CAGCAGTGTCTGAGAGCTGGGGAGAGAGTCTTTGGACCAACAAAGGTATGGTGAACACAC	4527				
Db	162	CAGCAGTGTCTGAGAGCTGGGGAGAGAGTCTTTGGACCAACAAAGGTATGGTGAACACAC	221			
4528	TTTCGCCCTTAATCTTAATGCGCAAGTGGAGAGAGGTTCGACGGGACAGAAATCCCTGGTT	4587				
Db	222	TTTCGCCCTTAATCTTAATGCGCAAGTGGAGAGAGGTTCGACGGGACAGAAATCCCTGGTT	281			

Query Match 5.7%; Score 612.8; DB 10; Length 691;
 Best Local Similarity 98.9%; Pred. No. 1.9e-76;
 Matches 617; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1397 TACAGCTGCTTAACTAGTTGACAGAGATTTGGCCCTAGTGTAGACAGAGTGTCT 1456
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 Db 691 TACAGCTGCTTAACTAGTTGACAGAGATTTGGCCCTAGTGTAGACAGAGTGTCT 632
 QY 1457 GTGGGTACACGCGGCGCTACACAGACACTTGAATTTGGTACTAGCTATGATCTTAAACAT 1516
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 Db 631 GTGGGTACACGCGGCGCTACACAGACACTTGAATTTGGTACTAGCTATGATCTTAAACAT 572
 QY 1517 TTTACACATGACAGAGATGAGCAGTGGCGCTGCTTCTGCGCAATTTATTCATATGG 1576
 |||||||
 Db 571 TTTACACATGACAGAGATGAGCAGTGGCGCTGCTTCTGCGCAATTTATTCATATGG 512
 QY 1577 TACAGTGGCTTTGGTGGGAGAGCTCATGTCTCCACTTCATAGCTATGATCTTAAACAT 1636
 |||||||
 Db 511 TACAGTGGCTTTGGTGGGAGAGCTCATGTCTCCACTTCATAGCTATGATCTTAAACAT 452
 QY 1637 CACACTGCATTTAGAGGTGATTAATTAATTAATTTGATTTGAGCAGAAATATTCATTTGTTA 1696
 |||||||
 Db 451 CACACTGCATTTAGAGGTGATTAATTAATTAATTTGATTTGAGCAGAAATATTCATTTGTTA 392
 QY 1697 CAAGTGAATGATGATGCGGCGCATGTGTGACCTGTCAAGGCCCAAGGAGAGAGAGAG 1756
 |||||||
 Db 391 CAAGTGAATGATGATGCGGCGCATGTGTGACCTGTCAAGGCCCAAGGAGAGAGAGAGAG 332
 QY 1757 GAAACAAGTCTTACCTTTGATTAATTTGATTTGATTTGATTTGAGGAGAGATGACATAAGCAA 1816
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 Db 331 GAAACAAGTCTTACCTTTGATTAATTTGATTTGATTTGAGGAGAGATGACATAAGCAA 272
 QY 1817 TGACGAGAAGATATPACATCAGAGAAATCATGGGTGTGTGAGAGACAGAGAGTGTAG 1876
 |||||||
 Db 271 TGACGAGAAGATATPACATCAGAGAAATCATGGGTGTGTGAGAGACAGAGAGTGTAG 212
 QY 1877 GGCAGATCACTGTGGGCTGACACTTGGACAGACATGAGAAATTAAGATGATATTTG 1936
 |||||||
 Db 211 GGCAGATCACTGTGGGCTGACACTTGGACAGACATGAGAAATTAAGATGATATTTG 152
 QY 1937 ACTGGAGAGATTTTCCAGGCAAACTGATGGGCTGGCAAGTTGATTAATTAAGAGCGG 1996
 |||||||
 Db 151 ACTGGAGAGATTTTCCAGGCAAACTGATGGGCTGGCAAGTTGATTAATTAAGAGCGG 92
 QY 1997 GTTTTCTCAGCACTACTCATGTGT 2020
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 Db 91 GTTTTCTCAGCGGCGCGGTGGGT 68

RESULT 2
 AG116246/c 648 bp DNA linear GSS 03-NOV-2001
 LOCUS AG116246 Pan troglodytes DNA, clone: PTB-123115.R, genomic survey sequence.
 DEFINITION AG116246
 ACCESSION AG116246.1 GI:16736765
 VERSION
 KEYWORDS GSS: GSS (genome survey sequence);
 SOURCE Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male
 ORGANISM BAC library clone:PTB-123115.R.
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (sites)
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE BAC end sequences of library PTB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 648)
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbasesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the Rad process and may have higher chance of
 clone tracking errors.
 PRIMERS

Sequencing: MJ3Rev
 LIBRARY

Vector : pRS145
 R.site 1 : SacI
 R.site 2 : SacI.

FEATURES
 source Location/Qualifiers

1..648
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-123115.R"
 /sex="male"
 /cell_type="lymphoblast"

BASE COUNT 212 a 148 c 125 g 163 t
 ORIGIN

Query Match 5.4%; Score 589; DB 12; Length 648;
 Best Local Similarity 99.2%; Pred. No. 4.2e-73;
 Matches 592; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 Db 648 GAGAGTCTCTAGGCTGGAGAGCTCCTGAGAGAGCTTACCTGGGCGCTTCCCACTCTT 589
 QY 1066 GGCATTTGTTCTTTGCGCGGAAATTAAGTATATGATTTGATTTGAGCGTTGAAGTGA 1125
 |||||||
 Db 588 GGCATTTGTTCTTTGCGCGGAAATTAAGTATATGATTTGATTTGAGCGTTGAAGTGA 529
 QY 1126 CAATTCCTTTTGGGCTTATTTGATTTGCAATGCTGTGTATTAAGAGGCTTC 1185
 |||||||
 Db 528 CAATTCCTTTTGGGCTTATTTGATTTGCAATGCTGTGTATTAAGAGGCTTC 469
 QY 1186 TCTACAAAGTACTGATTAATGACATGTAAAGCAATGCACTCACTCTTAAGTTACATTCATA 1245
 |||||||
 Db 468 TCTACAAAGTACTGATTAATGACATGTAAAGCAATGCACTCACTCTTAAGTTACATTCATA 409
 QY 1246 TCTGATCTTATTTGATTTTCACTAGGCAATGGAGAGTGAAGCTTAATTAATTAAGTTATTT 1305
 |||||||
 Db 408 TCTGATCTTATTTGATTTTCACTAGGCAATGGAGAGTGAAGCTTAATTAATTAAGTTATTT 349
 QY 1306 TACTAGAGTTAAGTGAATTCAGATTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1365
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 Db 348 TACTAGAGTTAAGTGAATTCAGATTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 289
 QY 1366 TAATCTGGATTTCTGATGTTATTTCAAGTACTACAGCTGCTTCAATCTTATTTAGACAGT 1425
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 Db 288 TAATCTGGATTTCTGATGTTATTTCAAGTACTACAGCTGCTTCAATCTTATTTAGACAGT 229
 QY 1426 GATTTGGCCCTGAGTGTGACAGAGTGTCTGTGGTACACGCGGCGCTGAGACAGCA 1485
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 Db 228 GATTTGGCCCTGAGTGTGACAGAGTGTCTGTGGTACACGCGGCGCTGAGACAGCA 169
 QY 1486 CTTTGAATTTGGTACTACAGTGTATTCACATTTTACACATGACAGAAATGAGGATGGCA 1545
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 Db 168 CTTTGAATTTGGTACTACAGTGTATTCACATTTTACACATGACAGAAATGAGGATGGCA 109
 QY 1546 CGGCGCTTCCCGGAAATTAATTCATGAGTACAGGCTGGCTTGGTGGCAGACCTC 1602
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 Db 108 CGGCGCTTCCCGGAAATTAATTCATGAGTACAGGCTGGCTTGGTGGCAGACCTC 52

RESULT 3
 AW974162/c 545 bp mRNA linear EST 02-JUN-2000
 LOCUS AW974162

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 13:30:58 ; Search time 7317.93 seconds

(without alignments)
19965.282 Million cell updates/sec

Title: us-09-497-957-1

Perfect score: 10825

Sequence: 1 TCTAAGCTTGAGATAAAT.....TCCCCAAATTTTCATTAAC 10825

Scoring table: IDENTITY_NUC

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	589	5.4	646	12	AG116246 Pan trogl
C 3	464.8	4.3	545	9	AW974162 EST86265
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C 8	423.4	3.9	520	9	A1949947 wq04f05.x
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ALIGNMENTS

RESULT 1	BG926549	691 bp	MRNA	linear	EST 06-NOV-2001
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ACCESSION	BG926549				
VERSION	BG926549.1	GI:14321072			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.				
TITLE	Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries				
JOURNAL MEDLINE	Osteoarthritis Cartilage 9 (7), 641-653 (2001)				
COMMENT	Contact: Sanjay Kumar				
	UM2109				
	GlaxoSmithKline				
	709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA				
	Tel: 610-270-7245				
	Fax: 610-270-5598				
	Email: sanjay_kumar-legsk.com				
	Seq primer: 77.				

FEATURES

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 13:57:28 ; Search time 174.74 Seconds
(without alignments)
15216.795 Million cell updates/sec

Title: US-09-497-957-1
Perfect score: 10825
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 363533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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US-08-652-265-1
Sequence 1, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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RESULT 2

US-08-652-265-3
 ; Sequence 3, Application US/08652265
 ; Patent No. 6025130

GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.
 ; APPLICANT: Drayna, Dennis T.
 ; APPLICANT: Feder, John N.
 ; APPLICANT: Guirke, Andreas
 ; APPLICANT: Ruddy, David
 ; APPLICANT: Tsuchihashi, Zenta
 ; APPLICANT: Wolff, Roger K.
 ; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/652,265
 ; FILING DATE: 23-MAY-1996
 ; CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 17957-000500
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10825 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
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 ; US-08-652-265-3

Query Match 100.0%; Score 10823; DB 3; Length 10825;
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 Db 121 TCAGGATTTAAAAACCAAGGGGACACCTGATCAGCTAGTGTTCACAAAGCAGGTACCTT 180

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Db	3061	CAGTGTAAAGAAATTCAGAGACAAGGCTGGGCACGSGTGGCTCACTTCTGTAAATCCCAGCACT	3120
Qy	3121	TTGGTGGCTGAGCAGGTAGATCATTTGAGGTGAGGAGTTTGAGCAGAGCTTTGGCCAAACA	3180
Db	3121	TTGGTGGCTGAGCAGGTAGATCATTTGAGGTGAGGAGTTTGAGCAGAGCTTTGGCCAAACA	3180
Qy	3181	TGSGTAAACCCCATGTCTACTAAAAATACAAAAATTAGCCCTGGTGGTGCGCGCACGCCCT	3240
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Qy	3241	ATAGTCCACAGTTTTCAGGAGGCTTAGTGAGAGAAATCCCTTGAACCCAGAGGTGCGAGG	3300
Db	3241	ATAGTCCACAGTTTTCAGGAGGCTTAGTGAGAGAAATCCCTTGAACCCAGAGGTGCGAGG	3300
Qy	3301	TTGCAGTGAGCTGAGATTTGCGCATGTCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
Db	3301	TTGCAGTGAGCTGAGATTTGCGCATGTCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
Qy	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTCAAGGAATTTATTCCTCAGGATTTTGGG	3420
Db	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTCAAGGAATTTATTCCTCAGGATTTTGGG	3420
Qy	3421	TCTAATTTGCCCTGAGACCAACTCCTGAGTTCAACTACCATGGCTAGACACACTTTAAC	3480
Db	3421	TCTAATTTGCCCTGAGACCAACTCCTGAGTTCAACTACCATGGCTAGACACACTTTAAC	3480
Qy	3481	ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTTGGAATAGAT	3540
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Db	3541	CTGGGGCAGTGAGGGGTGGCAGCCAGTCGTGGCAGAGAAAAGCACACAGGAAGAGC	3600

Qy	3601	ACCAGAC	TGTCATATGGAAGAACAGACAGACTGCAACTCACCCCTTCACAAAATGAGGA	3660
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Qy	3721	CTCCTACT	ACACATGGTTTAAGGCCTGTGCTCTGTCTCCAGGTTCAACACTCTCTGCACTA	3780
Db	3721	CTCCTACT	ACACATGGTTTAAGGCCTGTGCTCTGTCTCCAGGTTCAACACTCTCTGCACTA	3780
Qy	3781	CCTCTTCAT	GGGTGCCTTCAGACGAGCAACCTTGGTCTTTTCCCTTGTGTAAGCTTTTGGGCTA	3840
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Db	3901	TCCATGGG	TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCGAGTCAAGACTCTGAA	3960
Qy	3961	AGGCTGGG	ATCACATGTTCACTGTTGACCTTCGACTTCGACTATATGGAANAATCAACAACACAG	4020
Db	3961	AGGCTGGG	ATCACATGTTCACTGTTGACCTTCGACTTCGACTATATGGAANAATCAACAACACAG	4020
Qy	4021	CAAGGGT	ATGTGGAGAGGGGGCCTCACCTTCTCGAGTTGTCAAGCTTTTTCATCTTTTC	4080
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Qy	4141	GAATTTGC	TTCCCTGAGATCAATTTGGTCTCTGGGGATGGTGGAAATPAGGACCTATTCTTT	4200
Db	4141	GAATTTGC	TTCCCTGAGATCAATTTGGTCTCTGGGGATGGTGGAAATPAGGACCTATTCTTT	4200
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Qy	4321	CAGGACCA	CCCTTGAATTTCTGCCCTGACACACTTGGATTTGGAGACAGCAAGAACCACGGGCC	4380
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Qy	4441	CTGGAGAG	GGAAGCTGCCCTGCACAGCTGCAAGCTTGTCTGGAGCTGGGAGAGGTGTTTG	4500
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Qy	4501	GACCAACA	GAAGTATGGTGGGAACACACTTCTGCCCTTACTCTAGTGGGACAGATGGAGG	4560
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Qy	4561	AGGTTGCA	GGGCGGAATCCCTTGGTGTGAGTTTTCAGAGGTGGCTGAGGCTGTCTGCCTC	4620
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Qy	4621	TCCAAAT	TTCTGGGAAGGACTTTCTCAATCCCTAGAGTCTCTACCTTATPAAATGAGATGTA	4680
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Db	10141	CCAGTCTTCACAGTAACACATTTCACTAACACATTTACTAAACATCAGCACTGTGGCT	10200
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Db	10201	GTTAAATTTTTTAATAGAAATTTAAGTCCTCATTTCTTCGGTGTTTTTAAAGCTTAA	10260
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Db	10261	TTTTCTCGCTTTATTCATAAATCTTTAAGTCAACTACATTTGAAAATCAAGACCTG	10320
Qy	10321	CATTTTAAATTTCTTATTCACCTCTGGCAAAACCATTCACAACCATGGTAGTAAAGAAA	10380
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Db	10381	GGGTGACACCTGGTGGCCATAGGTAAATGTACACGGTGGTCCGGTGACCAGAGATGCAG	10440
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Db	10441	CGCTGAGGGTTTTCTCTGAAGGTAAAGGAATTAAGAATGGGTGGAGGGGGTGCACTGGAA	10500
Qy	10501	ATCACTTGTAGAGAAAGCCCTGAAATTTGAGAAACAAACAAGAAACTACTTACCAG	10560
Db	10501	ATCACTTGTAGAGAAAGCCCTGAAATTTGAGAAACAAACAAGAAACTACTTACCAG	10560
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Qy	10621	ANGGAAACAAACCACTCTGATTAATCATTTAGTCAAGTACAGCAGGTGATGTGAGACTGC	10680
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Qy	10681	TGAGAGGTACAGGCCAAAATTTCTATGTTGTTATTATAATATGTCATCTTATAATACTGT	10740
Db	10681	TGAGAGGTACAGGCCAAAATTTCTATGTTGTTATTATAATATGTCATCTTATAATACTGT	10740
Qy	10741	CAGTATTTTATAAATCTCTTCACAACTCACACATTTTAAACAAACCACTGTCTC	10800
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RESULT      3
US-08-652-265-5
; Sequence 5, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchinashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```


SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 17957-000500

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 10825 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,

LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis

OTHER INFORMATION:

OTHER INFORMATION: mutation"

OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)

OTHER INFORMATION: gene 24d2 allele"

FEATURE:

NAME/KEY: -

LOCATION: 140..7319

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"

FEATURE:

NAME/KEY: -

LOCATION: 3852..3891

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: genomic sequence surrounding variant

OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"

FEATURE:

NAME/KEY: -

LOCATION: 5507..6023

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: genomic sequence surrounding variant

OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"

FEATURE:

NAME/KEY: allele

LOCATION: replace(3872, "g")

OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis

OTHER INFORMATION:

OTHER INFORMATION: /label= 24d2

US-08-652-265-5

Query Match 100.0%; Score 10823; DB 3; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	121	TCAGGATTTAAACACCAAGGGGACACTGGATCACCTAGTGTTCACAACGAGTACCT	180
Db	121	TCAGGATTTAAACACCAAGGGGACACTGGATCACCTAGTGTTCACAACGAGTACCT	180
Qy	181	CTGCTGTAGGAGAGAGAACTAAAGTTCGAAAGACCTGCTTTTCCACGAGGAGTT	240
Db	181	CTGCTGTAGGAGAGAGAACTAAAGTTCGAAAGACCTGCTTTTCCACGAGGAGTT	240

Qy	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGAAGTCTTGGAGCCATCCCCG	300
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Db	361	ATGGGCGCGGAGCGAGCGGGGCTTCTCCTCTCTGATGCTTTTGCAGACCGCGGTCCTG	420
Qy	421	CAGGGCGCTTGTGCTGATGCTCGAGGCTCGGGGAACTAGGGCGCGGGGGTG	480
Db	421	CAGGGCGCTTGTGCTGATGCTCGAGGCTCGGGGAACTAGGGCGCGGGGGTG	480
Qy	481	GAAAAATCGAAACTAGCTTTTCTTTCGCTTGGAGTTTGCCTCTCTGATGCTTTTGCAGACCGCGGTCCTG	540
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Qy	601	CTACCAGTGAACTCAGATAGGGGCTCCCTCGCCCGAGGAGCTGCCCTCCCGGCTGT	660
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Qy	661	CCGGGCTCTCGGAGTGACTTTTGAACCGCCACCTCCCTCCCGCAACTAGAACTCTT	720
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Qy	901	GGTTCCACCTCAGAACGAAATGGGTTGGGCGCGGAGAGAGTGGCGTTGGGA	960
Db	901	GGTTCCACCTCAGAACGAAATGGGTTGGGCGCGGAGAGAGTGGCGTTGGGA	960
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Qy	1021	GGAGGCTCCTGAGAGGCTTACCTCGGGCTTTCCCGACTCTTGGCAATTTCTTTT	1080
Db	1021	GGAGGCTCCTGAGAGGCTTACCTCGGGCTTTCCCGACTCTTGGCAATTTCTTTT	1080
Qy	1081	GCTGTGAAATTAAGTATATGTTAGTTTGAAGTTGAACTGAACAATTTCTTTTGG	1140
Db	1081	GCTGTGAAATTAAGTATATGTTAGTTTGAAGTTGAACTGAACAATTTCTTTTGG	1140
Qy	1141	CTAGGCTTTTATTCATTTGCAATGCTGTGTAATTAAGAGGCTCTTACAAAGTACTGA	1200
Db	1141	CTAGGCTTTTATTCATTTGCAATGCTGTGTAATTAAGAGGCTCTTACAAAGTACTGA	1200
Qy	1201	TAAATGACATGTAAGCAATGCACTTCTAAGTTACATTCATCAATCTTATTTGA	1260
Db	1201	TAAATGACATGTAAGCAATGCACTTCTAAGTTACATTCATCAATCTTATTTGA	1260
Qy	1261	TTTTTCACTAGGAGGAGGAGGCTTAATTAACGTTTATTTTACTAGAGTTACT	1320
Db	1261	TTTTTCACTAGGAGGAGGAGGCTTAATTAACGTTTATTTTACTAGAGTTACT	1320

QY 5701 AAGTGGCTGAAGGATAAGCAGCCAAATGGATGCCAGGAGTTCGAACCTAAAGACCTATTG 5760
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RESULT 4
us-08-652-265-7
; Sequence 7, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
US-08-652-265-7

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RESULT 5
US-08-834-497A-1
; Sequence 1, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.

APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Guirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
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OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
US-08-834-497A-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 121 TCAGGATTTAAACCAAGGGGACACTGGATCACCCTAGTGTTCACACAGCAGGTACCTT 180
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAGACCTGTGTCTTTTCCACAGGAAGTT 240
Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAGACCTGTGTCTTTTCCACAGGAAGTT 240
QY 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGAGCATCCCG 300
Db 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGAGCATCCCG 300
QY 301 TTTTCCCGCCCCCAAGAGAGCGGAGATTTAAACGGGACGTGCGGCCAGAGCTGGGAA 360
Db 301 TTTTCCCGCCCCCAAGAGAGCGGAGATTTAAACGGGACGTGCGGCCAGAGCTGGGAA 360
QY 361 ATGGGCCCCGAGAGCAGCGCGCGCTTCTCCTCTGATGCTTTTCACACCGCGCTCTG 420
Db 361 ATGGGCCCCGAGAGCAGCGCGCGCTTCTCCTCTGATGCTTTTCACACCGCGCTCTG 420
QY 421 CAGGGCGCTTGTCTGCTGAGTCCGAGGCGTCCGGCGGAACCTAGGGCGCGCGGGGTG 480
Db 421 CAGGGCGCTTGTCTGCTGAGTCCGAGGCGTCCGGCGGAACCTAGGGCGCGCGGGGTG 480
QY 481 GAAAAATCGAAACTAGCTTTTCTTTGGCGCTGGGAGTTTGTAACTTTGGAGACCTGTC 540
Db 481 GAAAAATCGAAACTAGCTTTTCTTTGGCGCTGGGAGTTTGTAACTTTGGAGACCTGTC 540
QY 541 TCNACCCCTATCGCAGAGCCCTCTCCCTACTTTCTGCGCTCCAGACCCCGTGAGGAGTGC 600
Db 541 TCAACCCCTATCGCAGAGCCCTCTCCCTACTTTCTGCGCTCCAGACCCCGTGAGGAGTGC 600
QY 601 CTACCACCTGAACCTGCGAGATAGGGGTCCCTCGCCCGCAGGACCTGCCCCCTCCCGGCTGT 660

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Db 601 CTACCACTGAAGTGCAGATAGGGTCCCTCGCCCGCAGGACCTGCCCTCCCGCGGTGT 660
QY 661 CCCGGCTCTGGGAGTACCTTTTGAACCGCCACTCCCTTCCCGCACTAGATGCTTT 720
Db 661 CCCGGCTCTGGGAGTACCTTTTGAACCGCCACTCCCTTCCCGCACTAGATGCTTT 720
QY 721 TAAATAAATCTCGTAGTTCCTCCTCAGCTGAGCTAAGCCTGGGGCTCCCTTGAACCTGG 780
Db 721 TAAATAAATCTCGTAGTTCCTCCTCAGCTGAGCTAAGCCTGGGGCTCCCTTGAACCTGG 780
QY 781 AACTCGGGTTTATTTCCCAATGTCAGCTGCGAGTTTTCCTCCAGTCACTCCAAACAGG 840
Db 781 AACTCGGGTTTATTTCCCAATGTCAGCTGCGAGTTTTCCTCCAGTCACTCCAAACAGG 840
QY 841 AAGTTCTTCCCTCGAGTGTTCGCGAGAAGGCTGAGCAACCCACAGCAGGATCCGCAAG 900
Db 841 AAGTTCTTCCCTCGAGTGTTCGCGAGAAGGCTGAGCAACCCACAGCAGGATCCGCAAG 900
QY 901 GGTTCACACTCAGAACGATCGGTTGGCGGTGGGCGCGGAAGAGTGGCGTTGGGA 960
Db 901 GGTTCACACTCAGAACGATCGGTTGGCGGTGGGCGCGGAAGAGTGGCGTTGGGA 960
QY 961 TCTGAATCTTCAACATTCACCCACTTTTGGTGAGACCTGGGGTGGAGTCTCTAGGGT 1020
Db 961 TCTGAATCTTCAACATTCACCCACTTTTGGTGAGACCTGGGGTGGAGTCTCTAGGGT 1020
QY 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGGCTTTCCCGCACTCTGGCAATGTCTTTT 1080
Db 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGGCTTTCCCGCACTCTGGCAATGTCTTTT 1080
QY 1081 GCCTGGAATAATAGTATATGTAGTTTGAACGTTTGAACGTAACAAATCTCTTTTCGG 1140
Db 1081 GCCTGGAATAATAGTATATGTAGTTTGAACGTTTGAACGTAACAAATCTCTTTTCGG 1140
QY 1141 CTAGGCTTTATGATTTGCAATGTGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200
Db 1141 CTAGGCTTTATGATTTGCAATGTGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200
QY 1201 TAATGAACATGTAAGCAATGCACCTCACTTAAGTTACATTCATATCTGATCTTATTGA 1260
Db 1201 TAATGAACATGTAAGCAATGCACCTCACTTAAGTTACATTCATATCTGATCTTATTGA 1260
QY 1261 TTTTCTACTAGGATAGGAGGTAGGAGCTAAATACGTTTATTTTACTAGAAGTTAACT 1320
Db 1261 TTTTCTACTAGGATAGGAGGTAGGAGCTAAATACGTTTATTTTACTAGAAGTTAACT 1320
QY 1321 GGAATTCAGATTAATAACTCTTTTCAGGTTACAAGAACATAAATAATCTGGTTTCTG 1380
Db 1321 GGAATTCAGATTAATAACTCTTTTCAGGTTACAAGAACATAAATAATCTGGTTTCTG 1380
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTTAATCTTAGTTGACAGTGAATTTGCCCTGTAG 1440
Db 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTTAATCTTAGTTGACAGTGAATTTGCCCTGTAG 1440
QY 1441 TGTAGCACAGTGTCTGTGGTTCACACCGCGCTCAGCACAGCACTTTGAGTTTGTGA 1500
Db 1441 TGTAGCACAGTGTCTGTGGTTCACACCGCGCTCAGCACAGCACTTTGAGTTTGTGA 1500
QY 1501 CTAGCTGTATCCACATTTTACATACAGAAATGAGGCATGGCAGCGCTGCTTCCCTGG 1560
Db 1501 CTAGCTGTATCCACATTTTACATACAGAAATGAGGCATGGCAGCGCTGCTTCCCTGG 1560
QY 1561 CAAATTTATTCATGTAGTACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
Db 1561 CAAATTTATTCATGTAGTACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
QY 1621 TATGATTTTAAACATCACACTGCATTTAGAGTTGAATAATAAATTTTCATGTTGAGCAG 1680
Db 1621 TATGATTTTAAACATCACACTGCATTTAGAGTTGAATAATAAATTTTCATGTTGAGCAG 1680
QY 1681 AATATTTCTATGTTTCAAGTGTAAATGATCCCGCAATGTGTGCACTGTCTCAAGCCC 1740
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Db 1681 AATATTTCTATGTTTACAGTGTAAATGAGTCCAGCCATGTGTGCACTGTTCAAGCCC 1740
QY 1741 CAAGGGAGAGACAGGAAACAAAGTCTTTACCTTTTGATATTTTGGCATTTCTAGTGGGAGA 1800
Db 1741 CAAGGGAGAGACAGGAAACAAAGTCTTTACCTTTTGATATTTTGGCATTTCTAGTGGGAGA 1800
QY 1801 GATGACAATAGCAATAGCAGAGAAGATATACAACTACAGAAATCATGGGTGTTGTGA 1860
Db 1801 GATGACAATAGCAATAGCAGAGAAGATATACAACTACAGAAATCATGGGTGTTGTGA 1860
QY 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGAGACATGAAGGA 1920
Db 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGAGACATGAAGGA 1920
QY 1921 AATAAGAATGATATTGACTGGGAGCAGTATTTCOCAGGCAAACTAGTGGGCCCTGGCAAG 1980
Db 1921 AATAAGAATGATATTGACTGGGAGCAGTATTTCOCAGGCAAACTAGTGGGCCCTGGCAAG 1980
QY 1981 TTGGATTAAGGCGGGTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGG 2040
Db 1981 TTGGATTAAGGCGGGTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGG 2040
QY 2041 CGCGCTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTAGCAGTATCCTGT 2100
Db 2041 CGCGCTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTAGCAGTATCCTGT 2100
QY 2101 CCTCCCTACTCACTAGGTGCTAGGAGCAGTCCCCAGTCTTGACAACCAAAATGTCTCT 2160
Db 2101 CCTCCCTACTCACTAGGTGCTAGGAGCAGTCCCCAGTCTTGACAACCAAAATGTCTCT 2160
QY 2161 AAACCTTGCCACATGTCACCTAGTAGACAAACTCCTGCTTAAGAAGCTCGGGTTGAAAA 2220
Db 2161 AAACCTTGCCACATGTCACCTAGTAGACAAACTCCTGCTTAAGAAGCTCGGGTTGAAAA 2220
QY 2221 AATAACAAGTGTGCTGGGAGTAGAGGCCAAGAAAGTAGGTAATGGCTCAGAAAGGA 2280
Db 2221 AATAACAAGTGTGCTGGGAGTAGAGGCCAAGAAAGTAGGTAATGGCTCAGAAAGGA 2280
QY 2281 GCCACAAACAAGGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATTCAGCAAGGAGTA 2340
Db 2281 GCCACAAACAAGGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATTCAGCAAGGAGTA 2340
QY 2341 ACAGTCACTGTACAGGCTTTTAAAGATGCTCTGGCTGCTATGTGGAAAGCAGATG 2400
Db 2341 ACAGTCACTGTACAGGCTTTTAAAGATGCTCTGGCTGCTATGTGGAAAGCAGATG 2400
QY 2401 AAGGAGCAACAGTAAAAGCAGGAGCCAGCCAGGAGCTGTTACACAGTCCAGGCAAG 2460
Db 2401 AAGGAGCAACAGTAAAAGCAGGAGCCAGCCAGGAGCTGTTACACAGTCCAGGCAAG 2460
QY 2461 AGGTAGTGGAGTGGGCTGGGAGCAAGAAAGGAGTGACAAACCAATTTCTCTCTGAA 2520
Db 2461 AGGTAGTGGAGTGGGCTGGGAGCAAGAAAGGAGTGACAAACCAATTTCTCTCTGAA 2520
QY 2521 TATATTTCTGAAGAACTTCTGAAGGATCTATGTTGTGTGAGAGAAAGAAATGG 2580
Db 2521 TATATTTCTGAAGAACTTCTGAAGGATCTATGTTGTGTGAGAGAAAGAAATGG 2580
QY 2581 CTGGGTGTATGACTCATGCCAAGGAGGAGGCCAAGAGAGCAGATTCCTGAGCTCAGGA 2640
Db 2581 CTGGGTGTATGACTCATGCCAAGGAGGAGGCCAAGAGAGCAGATTCCTGAGCTCAGGA 2640
QY 2641 GTTCAAGACAGCCTGGGCAACACACAGCAAAACCCCTCTCTACAAAAATACAAAAATTA 2700
Db 2641 GTTCAAGACAGCCTGGGCAACACACAGCAAAACCCCTCTCTACAAAAATACAAAAATTA 2700
QY 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGAGGCTGAGGTGAGGTA 2760
Db 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGAGGCTGAGGTGAGGTA 2760
QY 2761 TTGCTTTGAGCCCAAGGAGTTGAGGCTGCAGTGCAGCCATGACTGTGCCACTGTACTTCAGC 2820
Db 2761 TTGCTTTGAGCCCAAGGAGTTGAGGCTGCAGTGCAGCCATGACTGTGCCACTGTACTTCAGC 2820

Db	4981	GCTAATTGGAAGGCTGAGCGAGGACATCCGCTTGAACCTTGGGAAGCGGAAGTTGCACATGA	5040
QY	5041	GCCAAAGATCGGCGCACTGCACATCCAGCCTTAGGCAGCAGAGTGGAGACTCCATCTTTAAAAA	5100
Db	5041	GCCAAAGATCGGCGCACTGCACATCCAGCCTAGGCAGCAGAGTGGAGACTCCATCTTTAAAAA	5100
QY	5101	AAAAAAGAGAGAAATTCAGAGATCTCAGACTATCATATCATATGAAATACAGAGACAAA	5160
Db	5101	AAAAAAGAGAGAAATTCAGAGATCTCAGACTATCATATCATATGAAATACAGAGACAAA	5160
QY	5161	ATATCAAGTGAAGCCACTTATCAGAGTGAAGAAATCCTTTAGGTTAAAAAGTTTCTTTCAT	5220
Db	5161	ATATCAAGTGAAGCCACTTATCAGAGTGAAGAAATCCTTTAGGTTAAAAAGTTTCTTTCAT	5220
QY	5221	AGACATAGCAATTAATCAGTGAAGCTTACCTATCTTACAAAGTCCCGTCTCTTATAACAATGC	5280
Db	5221	AGACATAGCAATTAATCAGTGAAGCTTACCTATCTTACAAAGTCCCGTCTCTTATAACAATGC	5280
QY	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAAATCAATTTCAATGACACATAA	5340
Db	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAAATCAATTTCAATGACACATAA	5340
QY	5341	AGGCCAATTTATCTATCAGAACAAAGACATGGGTAAACAGATATGATATATTACATGTG	5400
Db	5341	AGGCCAATTTATCTATCAGAACAAAGACATGGGTAAACAGATATGATATATTACATGTG	5400
QY	5401	AGGAGAACAAAGCTGATCTGACTCTCTCCAAAGTGACACTGTGTAGAGTCCCAATCTTAGG	5460
Db	5401	AGGAGAACAAAGCTGATCTGACTCTCTCCAAAGTGACACTGTGTAGAGTCCCAATCTTAGG	5460
QY	5461	ACACAAATGGTGCTCTCTCTGAGGTTGTTTTTCTGAAAAGGGTATTTTCCCTTCCTCC	5520
Db	5461	ACACAAATGGTGCTCTCTCTGAGGTTGTTTTTCTGAAAAGGGTATTTTCCCTTCCTCC	5520
QY	5521	AACCTATAGAAGGATGAAGTTCCAGTCTCCGCAAGGGTAAACAGATCCCTCTC	5580
Db	5521	AACCTATAGAAGGATGAAGTTCCAGTCTCCGCAAGGGTAAACAGATCCCTCTC	5580
QY	5581	CTCATCTCCTCTTTCCCTGTCAAGTGCCCTTTGGTGAAGGTGACACATCATGTGACC	5640
Db	5581	CTCATCTCCTCTTTCCCTGTCAAGTGCCCTTTGGTGAAGGTGACACATCATGTGACC	5640
QY	5641	TCCTCAGTGACCACTCTACGGTGTGGGCTTTGAACCTACTACCCCCAGAACATCACCATG	5700
Db	5641	TCCTCAGTGACCACTCTACGGTGTGGGCTTTGAACCTACTACCCCCAGAACATCACCATG	5700
QY	5701	AAAGTGGCTGAAGGATAAAGCAGCCATGGATGCCAAGGAGTTTCAAAGCTTAAAGACGTATTG	5760
Db	5701	AAAGTGGCTGAAGGATAAAGCAGCCATGGATGCCAAGGAGTTTCAAAGCTTAAAGACGTATTG	5760
QY	5761	CCCAATGGGATGGGACCTACCAAGGCTGGATGCCAAGGAGTTTCAAAGCTTAAAGACGTATTG	5820
Db	5761	CCCAATGGGATGGGACCTACCAAGGCTGGATGCCAAGGAGTTTCAAAGCTTAAAGACGTATTG	5820
QY	5821	CAGAGATATACGTCNCCAGGTGGAGCACCCAGGCTTGGATCAGCCCTCATTTGTGATCTGG	5880
Db	5821	CAGAGATATACGTCNCCAGGTGGAGCACCCAGGCTTGGATCAGCCCTCATTTGTGATCTGG	5880
QY	5881	GGTATGTGACTGATGAGACCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCC	5940
Db	5881	GGTATGTGACTGATGAGACCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCC	5940
QY	5941	TGAGGAGGTAATTTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGCTGGGCTCAGG	6000
Db	5941	TGAGGAGGTAATTTATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGCTGGGCTCAGG	6000
QY	6001	GTGCAATCAAGGCTTTTAACCTTGCTTTTCTGTGTTTAGAGCCCTCACCTCTGGCACCC	6060
Db	6001	GTGCAATCAAGGCTTTTAACCTTGCTTTTCTGTGTTTAGAGCCCTCACCTCTGGCACCC	6060
QY	6061	TAGTCATCTGGAGTCATCAGTGGAAATGCTGTTTTTGTCGTCATCTGTTCAATGGAATTT	6120
Db	6061	TAGTCATCTGGAGTCATCAGTGGAAATGCTGTTTTTGTCGTCATCTGTTCAATGGAATTT	6120

D	b	6061	TAGTCAATTCGGAGTCATCAGTGGAAATGCTGTCTTTTGTCGTCTCTTGTTCATTCGAATT	6120
Q	y	6121	TGTTCAATAAATTAAAGAACAGCAGGTTCAAGTGCAGTAGAACACAGGGGAAGTCTCT	6180
D	b	6121	TGTTCAATAAATTAAAGAACAGCAGGTTCAAGTGCAGTAGAACACAGGGGAAGTCTCT	6180
Q	y	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGCGACAGGGGATCTGGCATCCATGGG	6240
D	b	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGCGACAGGGGATCTGGCATCCATGGG	6240
Q	y	6241	AAGCATTTTTCTCATTTATATCTTTGGGACACAGCAGCTCCTGGGAGACAGAAAAT	6300
D	b	6241	AAGCATTTTTCTCATTTATATCTTTGGGACACAGCAGCTCCTGGGAGACAGAAAAT	6300
Q	y	6301	AATGGTTCTCCCCAGAATGAAGTCTTAATTCACAACAATCTTCAGAGCACCTACTAT	6360
D	b	6301	AATGGTTCTCCCCAGAATGAAGTCTTAATTCACAACAATCTTCAGAGCACCTACTAT	6360
Q	y	6361	TTTGCAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGTTGAGAATCTGTGGGTAT	6420
D	b	6361	TTTGCAGAGCTGTTTAAGGTAGTACAGGGGCTTTGAGTTGAGAATCTGTGGGTAT	6420
Q	y	6421	TCTCAGAACCCAAATCTGTTAGGGAATGAAATTTGATACAACTAAATCTAGTTAAAGAAG	6480
D	b	6421	TCTCAGAACCCAAATCTGTTAGGGAATGAAATTTGATACAACTAAATCTAGTTAAAGAAG	6480
Q	y	6481	ACCCCATGAGTCTTAAAGCAGCAGGAAGCAAATGCTTTAGGGTGTCAAAGGAAAGAAATG	6540
D	b	6481	ACCCCATGAGTCTTAAAGCAGCAGGAAGCAAATGCTTTAGGGTGTCAAAGGAAAGAAATG	6540
Q	y	6541	ATCACATTGAGCTGGGATCAAGATAGCCTCTGATAGTCTTCAAGAGGAAGCTGGATCCA	6600
D	b	6541	ATCACATTGAGCTGGGATCAAGATAGCCTCTGATAGTCTTCAAGAGGAAGCTGGATCCA	6600
Q	y	6601	TTAGGTGAGGTTGAGATGATGGAGGTCACACAGACGAGCAACCATGCCAAGTAGGA	6660
D	b	6601	TTAGGTGAGGTTGAGATGATGGAGGTCACACAGACGAGCAACCATGCCAAGTAGGA	6660
Q	y	6661	GAGTATAAGGCATACTGGGAGATTAGAATAATTACTGATCTTAAACCTGAGTTGCGT	6720
D	b	6661	GAGTATAAGGCATACTGGGAGATTAGAATAATTACTGATCTTAAACCTGAGTTGCGT	6720
Q	y	6721	AGCTATCACTACCAATATTGCTATTTACCCCCTGAACATCTGTGGTGTAGGAAAAAGA	6780
D	b	6721	AGCTATCACTACCAATATTGCTATTTACCCCCTGAACATCTGTGGTGTAGGAAAAAGA	6780
Q	y	6781	GAATCAGAAAGACCGACTCATACAGAGTCCAGGGTCTTTTCGGATATTGGTTATGA	6840
D	b	6781	GAATCAGAAAGACCGACTCATACAGAGTCCAGGGTCTTTTCGGATATTGGTTATGA	6840
Q	y	6841	TCACTGGGGTGTCATTGAAGGATCTTAAGAAAGGAGGACCAACGATCTTATATGGTG	6900
D	b	6841	TCACTGGGGTGTCATTGAAGGATCTTAAGAAAGGAGGACCAACGATCTTATATGGTG	6900
Q	y	6901	AATGCTGTGTAGAAAGTTAGATGAGAGGTGAGGAGACCAGTATAGAAGCCATATAGCAT	6960
D	b	6901	AATGCTGTGTAGAAAGTTAGATGAGAGGTGAGGAGACCAGTATAGAAGCCATATAGCAT	6960
Q	y	6961	TTCCAGATGAGAGATAATGGTTCTTGAATCCAATAGTGCACAGGCTTAATTTAGATGG	7020
D	b	6961	TTCCAGATGAGAGATAATGGTTCTTGAATCCAATAGTGCACAGGCTTAATTTAGATGG	7020
Q	y	7021	GTGAATTAGGAAAATAAGGAAGAGAGAGCGAAGATGGTGGCTAGGTTGTGATGCCCT	7080
D	b	7021	GTGAATTAGGAAAATAAGGAAGAGAGAGCGAAGATGGTGGCTAGGTTGTGATGCCCT	7080
Q	y	7081	CTTTCTCGGTCTCTTGCTCCACAGGAGGACCATGGGCATCTAGCTCTTACCTCAAG	7140
D	b	7081	CTTTCTCGGTCTCTTGCTCCACAGGAGGACCATGGGCATCTAGCTCTTACCTCAAG	7140
Q	y	7141	TGAGTGACACGAGCGCTGCAGACTCTGTTGGGAAGGAGACAAACTTAGAGACTCAAGA	7200
D	b	7141	TGAGTGACACGAGCGCTGCAGACTCTGTTGGGAAGGAGACAAACTTAGAGACTCAAGA	7200

QY 7201 GGGAGTCCATTTATGAGCTCTTCATGTTTCAGSAGAGAGTTGAACCTAAACATAGAAATT 7260
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Db 7201 GGGAGTGCAATTTATGAGCTCTTCATGTTTCAGSAGAGAGTTGAACCTAAACATAGAAATT 7260
QY 7261 GCCTGACGAACTCCTTGATTTTAGCCCTCTCTGTTTCATTTCCCTCAAAAAGATTTCCCCAT 7320
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Db 7261 GCCTGACGAACTCCTTGATTTTAGCCCTCTCTGTTTCATTTCCCTCAAAAAGATTTCCCCAT 7320
QY 7321 TTAGGTTTCTGAGTTCCTGATGCCGGTGATCCCTAGCTGTGACCTCTCCCTCGNACTG 7380
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Db 7321 TTAGGTTTCTGAGTTCCTGATGCCGGTGATCCCTAGCTGTGACCTCTCCCTCGNACTG 7380
QY 7381 TCTCTCATGAACCTCAAGCTGCACTATGAGGCTTCCTTCATTTCCCTCCCTCACTCAGAG 7440
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Db 7381 TCTCTCATGAACCTCAAGCTGCACTATGAGGCTTCCTTCATTTCCCTCCCTCACTCAGAG 7440
QY 7441 ACATACACCTATGCTATTTCAATTCCTATTTTGGAGGAGACTCCTTAAATTTGGGGGA 7500
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Db 7441 ACATACACCTATGCTATTTCAATTCCTATTTTGGAGGAGACTCCTTAAATTTGGGGGA 7500
QY 7501 CTTACATGATTCATTTTAACATCTGAGAAAGCTTTGAACCTGGGACCTGGCTAGTCAT 7560
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Db 7501 CTTACATGATTCATTTTAACATCTGAGAAAGCTTTGAACCTGGGACCTGGCTAGTCAT 7560
QY 7561 AACCTTACCAGATTTTACACATGTATCTATGCAATTTCTGGACCCGTTCAACTTTTCTCT 7620
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Db 7561 AACCTTACCAGATTTTACACATGTATCTATGCAATTTCTGGACCCGTTCAACTTTTCTCT 7620
QY 7621 TTGAATCCTCTCTGTTTACCAGTAAGCTATCTGTACCAAGCTTTGGGATTTCTTC 7680
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Db 7621 TTGAATCCTCTCTGTTTACCAGTAAGCTATCTGTACCAAGCTTTGGGATTTCTTC 7680
QY 7681 CATCTGATTTGATGTCAGTTGACAGCTATGAAGCTGTACACTGCACGAATGGAAGAG 7740
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Db 7681 CATCTGATTTGATGTCAGTTGACAGCTATGAAGCTGTACACTGCACGAATGGAAGAG 7740
QY 7741 GCACCTCTCCAGAAAAAGCATATGSGCTATCTGTGGTATGATGAGTGGTGTATTTAGC 7800
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Db 7741 GCACCTCTCCAGAAAAAGCATATGSGCTATCTGTGGTATGATGAGTGGTGTATTTAGC 7800
QY 7801 AGGTAGAGGCAATATCTTGAAGGGGTTGTAAGAGGTTTTCCTAATTTGGCATGA 7860
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Db 7801 AGGTAGAGGCAATATCTTGAAGGGGTTGTAAGAGGTTTTCCTAATTTGGCATGA 7860
QY 7861 AGGTGTCATACAGATTTGCAAAAGTTTAAATGGTCCTTCATTTGGGATGCTACTAGTAT 7920
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Db 7861 AGGTGTCATACAGATTTGCAAAAGTTTAAATGGTCCTTCATTTGGGATGCTACTAGTAT 7920
QY 7921 TCCAGACCTGAAGAATCACAAATATTTTACCTGCTCTCTCCTTGTCTGATAATGA 7980
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Db 7921 TCCAGACCTGAAGAATCACAAATATTTTACCTGCTCTCTCCTTGTCTGATAATGA 7980
QY 7981 ATTATGATAGGATGATAAAGCACTTACTTCGFTCCGACTCTTCCTGACACCTACTTA 8040
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Db 7981 ATTATGATAGGATGATAAAGCACTTACTTCGFTCCGACTCTTCCTGACACCTACTTA 8040
QY 8041 CATGCATTTACTGCATCTTTACAATAATCTATGAGATAGGTACTATATPCCCAT 8100
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Db 8041 CATGCATTTACTGCATCTTTACAATAATCTATGAGATAGGTACTATATPCCCAT 8100
QY 8101 TTCCTTTTAAATGAAGAAAGTGAAGTAGGCGGGGACGGTGGCTACGCTGTAATCCC 8160
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Db 8101 TTCCTTTTAAATGAAGAAAGTGAAGTAGGCGGGGACGGTGGCTACGCTGTAATCCC 8160
QY 8161 AGCACTTTGGGAGGCAAGCGGGTGGATCACGAGGTGAGAGATCGAGACCATCTCTGGC 8220
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Db 8161 AGCACTTTGGGAGGCAAGCGGGTGGATCACGAGGTGAGAGATCGAGACCATCTCTGGC 8220
QY 8221 TAACATGGTGAACCCCATCTCTTAATAAAAAACAAAAATTAAGCTGGGGTGGTGGCAG 8280
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Db 8221 TAACATGGTGAACCCCATCTCTTAATAAAAAACAAAAATTAAGCTGGGGTGGTGGCAG 8280

QY 8281 ACGCCTCTAGTCCAGCTACTCTCGAAGGCTGAGCGAGAGAAATGGCATGAACCCAGGAG 8340
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Db 8281 ACGCCTCTAGTCCAGCTACTCTCGAAGGCTGAGCGAGAGAAATGGCATGAACCCAGGAG 8340
QY 8341 CAGAGCTTGCACTGAGCGGAGTTTGGCCCACTGCACCTCCAGCTAGCTGACAGAGTCAGA 8400
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Db 8341 CAGAGCTTGCACTGAGCGGAGTTTGGCCCACTGCACCTCCAGCTAGCTGACAGAGTCAGA 8400
QY 8401 CTCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 8460
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Db 8401 CTCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 8460
QY 8461 TAGAGTATCTCATAGTTTGTGAGTAGAACAAGGTTTCAAACTCAGTCAATCTGACCG 8520
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Db 8461 TAGAGTATCTCATAGTTTGTGAGTAGAACAAGGTTTCAAACTCAGTCAATCTGACCG 8520
QY 8521 TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGATAAATAGAGAA 8580
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Db 8521 TTTGATACATCTCAGACACCACTACATTCAGTAGTTTAGATGCCTAGATAAATAGAGAA 8580
QY 8581 GGAAGGAGATGCTCTCTCTTGTCTCATTTGTTCTTCTGAGTGAAGTGAATCAAT 8640
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Db 8581 GGAAGGAGATGCTCTCTCTTGTCTCATTTGTTCTTCTGAGTGAAGTGAATCAAT 8640
QY 8641 GAAGGGGAACGAGAAACCAACCACTGATCCTCAGCTGTCTGATTTCCCTTAAAGTC 8700
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Db 8641 GAAGGGGAACGAGAAACCAACCACTGATCCTCAGCTGTCTGATTTCCCTTAAAGTC 8700
QY 8701 CCGTGAAGGAAGTCCCTGGAATGTGACTCCCTTGCTCTCTCTCTCTCTCTCTCTCTCT 8760
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Db 8701 CCGTGAAGGAAGTCCCTGGAATGTGACTCCCTTGCTCTCTCTCTCTCTCTCTCTCTCT 8760
QY 8761 TTTCTTTTGGACCTACGCAAGGACTGTAAATGGTGGGGACAGCTAGTGGCCCTGCTGGGC 8820
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Db 8761 TTTCTTTTGGACCTACGCAAGGACTGTAAATGGTGGGGACAGCTAGTGGCCCTGCTGGGC 8820
QY 8821 TTCACACAGGTGCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGCTGTTATTTTC 8880
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Db 8821 TTCACACAGGTGCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGCTGTTATTTTC 8880
QY 8881 CCTCAATGAAGTGGAGTAAAGCTCTCTCAATTTTGAGATGGTATTAATGGAAGCCACCAAGT 8940
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Db 8881 CCTCAATGAAGTGGAGTAAAGCTCTCTCAATTTTGAGATGGTATTAATGGAAGCCACCAAGT 8940
QY 8941 GCTTAGAGATGCCAGGTCCTTCCATGGAGCCACTGGGTTCCGGTCCGATCAATTAATA 9000
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Db 8941 GCTTAGAGATGCCAGGTCCTTCCATGGAGCCACTGGGTTCCGGTCCGATCAATTAATA 9000
QY 9001 AAAATCTAACCAAGGACATTCAGAAATTTGCTAGATTTCTGGGAAATCAGTTCCACATGTTCA 9060
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Db 9001 AAAATCTAACCAAGGACATTCAGAAATTTGCTAGATTTCTGGGAAATCAGTTCCACATGTTCA 9060
QY 9061 AAAGAGCTTTTTTTTTTTTTTTTGTGAGACTATTTGCCAGGCTGGAGTGCATATGAT 9120
|||||
Db 9061 AAAGAGCTTTTTTTTTTTTTTTTGTGAGACTATTTGCCAGGCTGGAGTGCATATGAT 9120
QY 9121 CTCGGCTCTACTGTAACTCTGCCCTCCAGGTTCAAGCAATTTCTCTGCTCAGCCCTCCCA 9180
|||||
Db 9121 CTCGGCTCTACTGTAACTCTGCCCTCCAGGTTCAAGCAATTTCTCTGCTCAGCCCTCCCA 9180
QY 9181 AGTAGCTGGGATTTACAGGCTGCACCAACCATGCCCGGCTFAATTTTGTATTTTGTAGTA 9240
|||||
Db 9181 AGTAGCTGGGATTTACAGGCTGCACCAACCATGCCCGGCTFAATTTTGTATTTTGTAGTA 9240
QY 9241 GACAGGTTTTCACCATTTTGGCCAGGCTGGTCTCGAACTCTCTGACCTCGTGATCCGCC 9300
|||||
Db 9241 GACAGGTTTTCACCATTTTGGCCAGGCTGGTCTCGAACTCTCTGACCTCGTGATCCGCC 9300
QY 9301 TGCCTCGGCTCCCAAGTGTGAGATTACAGTGTGAGCCACCTGCCAGCCGCTCAAA 9360
|||||
Db 9301 TGCCTCGGCTCCCAAGTGTGAGATTACAGTGTGAGCCACCTGCCAGCCGCTCAAA 9360
QY 9361 AGAGTCTTAATATATATATCCAGATGSCATGTTTGTACTTTTATGTTACTACATGCACTTG 9420

Db 9361 AGAGTCTTAATATATATATCCAGATGGCATGGTTTACTTTATGTACTACATGCCTTG 9420
QY 9421 GCTGCATAAATGCTGTACAGCAATCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT 9480
Db 9421 GCTGCATAAATGCTGTACAGCAATCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATAT 9480
QY 9481 ACAGCTCAGAACTTCTCTTTAGGCAATTAATTTAGCAAGATATCTCATCTCTCTT 9540
Db 9481 ACAGCTCAGAACTTCTCTTTAGGCAATTAATTTAGCAAGATATCTCATCTCTTCTT 9540
QY 9541 TTAACCAATTTCTTTTTTGTGGTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 9600
Db 9541 TTAACCAATTTCTTTTTTGTGGTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 9600
QY 9601 AGCCTCATTTGTAGAAAAGCTATAAATGAATACAAATTAAGCTGTATTTAATTAGCCAG 9660
Db 9601 AGCCTCATTTGTAGAAAAGCTATAAATGAATACAAATTAAGCTGTATTTAATTAGCCAG 9660
QY 9661 TGA AAAA ACTATTAAACAACCTGTCTATTACCTGTTAGTATTATTGTGCATTA AAAAATGCA 9720
Db 9661 TGA AAAA ACTATTAAACAACCTGTCTATTACCTGTTAGTATTATTGTGCATTA AAAAATGCA 9720
QY 9721 TATACCTTTAATAAATGATATATTTGATGTATCTACTGCATGATTTTATTTGAAGTTCTTGTTC 9780
Db 9721 TATACCTTTAATAAATGATATATTTGATGTATCTACTGCATGATTTTATTTGAAGTTCTTGTTC 9780
QY 9781 ATCTTGTGTATATACCTTAATCGCTTTGTCATTTTGGAGACATTTATTTTGTCTCTAATTT 9840
Db 9781 ATCTTGTGTATATACCTTAATCGCTTTGTCATTTTGGAGACATTTATTTTGTCTCTAATTT 9840
QY 9841 CTTTACATTTTGTCTTACGGAATATTTTCAATCAACTGTGTAGCGAAATTAATCGTGT 9900
Db 9841 CTTTACATTTTGTCTTACGGAATATTTTCAATCAACTGTGTAGCGAAATTAATCGTGT 9900
QY 9901 TCTTCACCTAGGACATTTGCTCTAGTTGTAAGCAATTTGTTTACACAGCAAAAC 9960
Db 9901 TCTTCACCTAGGACATTTGCTCTAGTTGTAAGCAATTTGTTTACACAGCAAAAC 9960
QY 9961 CATCTGAAAGCATATGACAAATTTTCTCTCTTAATATCTTACTATCTGAAAGCAGA 10020
Db 9961 CATCTGAAAGCATATGACAAATTTTCTCTCTTAATATCTTACTATCTGAAAGCAGA 10020
QY 10021 CTGCTATAAGGCTTCACTTACTCTTACCTCAATCAAGCAATGTTTACAATTAATTTATT 10080
Db 10021 CTGCTATAAGGCTTCACTTACTCTTACCTCAATCAAGCAATGTTTACAATTAATTTATT 10080
QY 10081 AGGTAAGCATTTGTTTATATTTGTTTATTTTACCTGGGTGAGATTTCAAGAAACACC 10140
Db 10081 AGGTAAGCATTTGTTTATATTTGTTTATTTTACCTGGGTGAGATTTCAAGAAACACC 10140
QY 10141 CCAGTCTTACAGTAACACATTTTCACTAACACATTTTACTAACATCAGCAACTGTGGCCT 10200
Db 10141 CCAGTCTTACAGTAACACATTTTCACTAACACATTTTACTAACATCAGCAACTGTGGCCT 10200
QY 10201 GTTAATTTTATAGAAATTTTAAAGTCTCATTTTCTTCGGTGTGTTTTTAAGCTTAA 10260
Db 10201 GTTAATTTTATAGAAATTTTAAAGTCTCATTTTCTTCGGTGTGTTTTTAAGCTTAA 10260
QY 10261 TTTTCTTGGCTTTATTCATAAATTTTAAAGTCAACTACATTTTGAAATTAAGACCTG 10320
Db 10261 TTTTCTTGGCTTTATTCATAAATTTTAAAGTCAACTACATTTTGAAATTAAGACCTG 10320
QY 10321 CATTTTAAATTTCTTATTCACCTCTGCGAAACCATTCACAAACCATGTTAGTAAAGAGAA 10380
Db 10321 CATTTTAAATTTCTTATTCACCTCTGCGAAACCATTCACAAACCATGTTAGTAAAGAGAA 10380
QY 10381 GGGTGACACCTGGTGGCCATAGTAAATGTACACAGTGTGCTGGTGACAGAGATGCGAG 10440
Db 10381 GGGTGACACCTGGTGGCCATAGTAAATGTACACAGTGTGCTGGTGACAGAGATGCGAG 10440
QY 10441 CGCTGAGGTTTTCTCTGAAGGTAAGGAATAAGAAATGGGTGGAGGGCGCTGCACCTGGAA 10500
Db 10441 CGCTGAGGTTTTCTCTGAAGGTAAGGAATAAGAAATGGGTGGAGGGCGCTGCACCTGGAA 10500

QY 10501 ATCACTTTAGAGAAAAAGCCCTCGAAAAATTTGAAAAACAAAAAGAAACTACTTACCAG 10560
Db 10501 ATCACTTTAGAGAAAAAGCCCTCGAAAAATTTGAAAAACAAAAAGAAACTACTTACCAG 10560
QY 10561 CTATTTCAATTTGCTGGAAATCACAGGCCATTTGCTGAGCTGCCTGAACTGGGAACACACAG 10620
Db 10561 CTATTTCAATTTGCTGGAAATCACAGGCCATTTGCTGAGCTGCCTGAACTGGGAACACACAG 10620
QY 10621 AAGAAAAACAAACCACTCTCTGATAATCATTCAGTCAAGTACAGCAGGTGATTGAGGACTGC 10680
Db 10621 AAGAAAAACAAACCACTCTCTGATAATCATTCAGTCAAGTACAGCAGGTGATTGAGGACTGC 10680
QY 10681 TGAGAGGTACAGGCCAAATTTCTTATTTATTAATAATGTCATCTTATAATACTGT 10740
Db 10681 TGAGAGGTACAGGCCAAATTTCTTATTTATTAATAATGTCATCTTATAATACTGT 10740
QY 10741 CAGTATTTTATAAAACATTTCTTCACAACTCACACACATTTAAAAACAAACACTGCTC 10800
Db 10741 CAGTATTTTATAAAACATTTCTTCACAACTCACACACATTTAAAAACAAACACTGCTC 10800
QY 10801 TAAATCCCCAAATTTTTCATAAAC 10825
Db 10801 TAAATCCCCAAATTTTTCATAAAC 10825

RESULT 6
US-08-834-497A-3
; Sequence 3, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999

Qy	1441	TGTAGCAGAGTGTCTGTGGGTGCACAGCGCGCCTCAGCAGACACTTTTGAGTTTTGGTA	1500
Db	1441	TGTAGCAGAGTGTCTGTGGGTGCACAGCGCGCCTCAGCAGACACTTTTGAGTTTTGGTA	1500
Qy	1501	CTAGCTGTATCCACATTTTACACATGACAAGAATGAGCATTGGCAGCGCTGCTTCCTCG	1560
Db	1501	CTAGCTGTATCCACATTTTACACATGACAAGAATGAGCATTGGCAGCGCTGCTTCCTCG	1560
Qy	1561	CAAAATTTATTTCAATAGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATAGC	1620
Db	1561	CAAAATTTATTTCAATAGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATAGC	1620
Qy	1621	TATGATTTCTTAAACATCACACTGCATTAGAGGTTCAAAATAATAAAATTTCAATGTTGAGCAG	1680
Db	1621	TATGATTTCTTAAACATCACACTGCATTAGAGGTTCAAAATAATAAAATTTCAATGTTGAGCAG	1680
Qy	1681	AAATATTATTGTTTAAAGTGTAAATGAGTCCCAAGCCATGTGTGCACCTGTTCACGCC	1740
Db	1681	AAATATTATTGTTTAAAGTGTAAATGAGTCCCAAGCCATGTGTGCACCTGTTCACGCC	1740
Qy	1741	CAGGGAGAGACAGCGGAACAAGTCTTTACCCCTTTGATATTTTGCATTTCTAGTGGGAGA	1800
Db	1741	CAGGGAGAGACAGCGGAACAAGTCTTTACCCCTTTGATATTTTGCATTTCTAGTGGGAGA	1800
Qy	1801	GATGACAATAAGCAAAATGAGCAGAGAAGATATACAACATCAGGAATCATGGTGTCTGTGA	1860
Db	1801	GATGACAATAAGCAAAATGAGCAGAGAAGATATACAACATCAGGAATCATGGTGTCTGTGA	1860
Qy	1861	GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGCTTGACATTTGAGCAGAGACATGAAGGA	1920
Db	1861	GAAGCAGAGAAGTCAGGGCAAGTCACTCTGGGCTTGACATTTGAGCAGAGACATGAAGGA	1920
Qy	1921	AATAAGAAATCATATTGACCTGGGAGCAGTATTTCCAGGCAAACTGAGTGGSCCTGGCAAG	1980
Db	1921	AATAAGAAATCATATTGACCTGGGAGCAGTATTTCCAGGCAAACTGAGTGGSCCTGGCAG	1980
Qy	1981	TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGGG	2040
Db	1981	TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGGG	2040
Qy	2041	CGCGCTGGGGTGGGAAGGGGACATACCATCTGCATGTAGCATGCTTAGCAGATATCCTGT	2100
Db	2041	CGCGCTGGGGTGGGAAGGGGACATACCATCTGCATGTAGCATGCTTAGCAGATATCCTGT	2100
Qy	2101	CCTCCCTACTCTAGGTGCTTAGGAGCACTCCCCAGTCTTGACAACCAAAAAATGCTCT	2160
Db	2101	CCFCCCTACTCTAGGTGCTTAGGAGCACTCCCCAGTCTTGACAACCAAAAAATGCTCT	2160
Qy	2161	AAACTTTGCCACATGTCACCTAGTAGACAAACTCTGGTTAAGAGCTCGGGTTGA AAAA	2220
Db	2161	AAACTTTGCCACATGTCACCTAGTAGACAAACTCTGGTTAAGAGCTCGGGTTGA AAAA	2220
Qy	2221	AATAAAACAAGTAGTCTGGGGAGTAGAGCCCAAGAAGTAGTAAATGGCCTCAGAAAGGA	2280
Db	2221	AATAAAACAAGTAGTCTGGGGAGTAGAGCCCAAGAAGTAGTAAATGGCCTCAGAAAGGA	2280
Qy	2281	GCCACAAAACAAGTTGTGCAGCGCCTGTAGSGTGTGGTGTGAATTTCTAGCCAAGGAGTA	2340
Db	2281	GCCACAAAACAAGTTGTGCAGCGCCTGTAGSGTGTGGTGTGAATTTCTAGCCAAGGAGTA	2340
Qy	2341	ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGAAGCAGAAATG	2400
Db	2341	ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGAAGCAGAAATG	2400
Qy	2401	AAGGGAGCAACAGTTAAAGCAGGGAGCCAGCCAGGAAGCTGTTTACAGATCCAGGCAAG	2460
Db	2401	AAGGGAGCAACAGTTAAAGCAGGGAGCCAGCCAGGAAGCTGTTTACAGATCCAGGCAAG	2460
Qy	2461	AGGTAGTGGAGTGGCTGGGTGGGAACAGAAAAGGAGTGACAAACCATTTGCTCTCGTGA	2520
Db	2461	AGGTAGTGGAGTGGCTGGGTGGGAACAGAAAAGGAGTGACAAACCATTTGCTCTCGTGA	2520
Qy	2521	TATATTCTGAAGGAAGTTGCTCAGAGGATTTCTATGTGTGTGAGAGAAGAGAAATTTGG	2580

D	b	2521	TATATTCTGAAGAAGTTGCTGAAGATTCTATGTGTGAGAGAAAGAGAATTTGG	2580
Q	y	2581	CTGGGTCTAGTACTCATGCCAAGGAGGAGGCCCAAGGACAGCAGATTCTCGAGTCAGGA	2640
D	b	2591	CTGGGTGTAGTAGTCTCATGCCAAGGAGGAGGCCAAGGACAGCAGATTCTCGAGTCAGGA	2640
Q	y	2641	GTTCAAGACCAGCGCTGGCCAACACAGCAAAAACCCCTTCTCTACAAAAATAACAANAATTA	2700
D	b	2641	GTTCAAGACCAGCGCTGGCCAACACAGCAAAAACCCCTTCTCTACAAAAATAACAANAATTA	2700
Q	y	2701	GCTGGGTGTGGTGCGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGTGGAGGGTA	2760
D	b	2701	GCTGGGTGTGGTGCGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGTGGAGGGTA	2760
Q	y	2761	TTGCTTTCAGGCCACAGGAAGTTGAGGCTGCAGTCGAGCGCATGACTGCCACTGTACTTTCAGC	2820
D	b	2761	TTGCTTTCAGGCCACAGGAAGTTGAGGCTGCAGTCGAGCGCATGACTGCCACTGTACTTTCAGC	2820
Q	y	2821	CTAGGTGACAGACAGACCCCTGTCTCCCTGACCCCCGTGAAAAGAGAGAGATTAAAGT	2880
D	b	2821	CTAGGTGACAGACAGACCCCTGTCTCCCTGACCCCCGTGAAAAGAGAGAGATTAAAGT	2880
Q	y	2881	TGACTTTGTTCTTTATTTTAAATTTTATTCGSCCTGAGCAGTGGGTAAATTCGCAATGCCAT	2940
D	b	2881	TGACTTTGTTCTTTATTTTAAATTTTATTCGSCCTGAGCAGTGGGTAAATTCGCAATGCCAT	2940
Q	y	2941	TTCTGAGATGGTGAAGCGACAGAGAAAGACAGTTTGGGTAAATCAAGSATCTGCATTTG	3000
D	b	2941	TTCTGAGATGGTGAAGCGACAGAGAAAGACAGTTTGGGTAAATCAAGSATCTGCATTTG	3000
Q	y	3001	GGACATCTTAAGTTTGAGATTCCAGTTCAGCTGAGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
D	b	3001	GGACATCTTAAGTTTGAGATTCCAGTTCAGCTGAGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
Q	y	3061	CAGTGTAAAGAAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACCT	3120
D	b	3061	CAGTGTAAAGAAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCCAGCACCT	3120
Q	y	3121	TTGGTGGCTCAGCAGGTAGATCAATTTGAGTTCAGGTTTGAGCAGAGCTTTGAGCAGAGCTTGGCCAAACA	3180
D	b	3121	TTGGTGGCTCAGCAGGTAGATCAATTTGAGTTCAGGTTTGAGCAGAGCTTTGAGCAGAGCTTGGCCAAACA	3180
Q	y	3181	TGSGTAAACCCCATGTCTACTAAAAATACAAAAAATTAGCTCGTGTGGTGGCGCACGCTCT	3240
D	b	3181	TGSGTAAACCCCATGTCTACTAAAAATACAAAAAATTAGCTCGTGTGGTGGCGCACGCTCT	3240
Q	y	3241	ATAGTCCCAGGTTTTTCAGGAGGCTTAGGTAGAGAAATCCCTTGAACCCAGGAGGTGCAGG	3300
D	b	3241	ATAGTCCCAGGTTTTTCAGGAGGCTTAGGTAGAGAAATCCCTTGAACCCAGGAGGTGCAGG	3300
Q	y	3301	TTGCAGTGCAGCTGAGATTGTGCCACTGCACTCCAGCTGGGTGATAGAGTGAGAGACTCTGT	3360
D	b	3301	TTGCAGTGCAGCTGAGATTGTGCCACTGCACTCCAGCTGGGTGATAGAGTGAGAGACTCTGT	3360
Q	y	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTTATTCCTCAGGATTTGGG	3420
D	b	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATTTATTCCTCAGGATTTGGG	3420
Q	y	3421	TCTAAATTTGCCCTGAGCACCACTCTCTGAGTTCAACTACCATGGCTAGACACCTTTAAC	3480
D	b	3421	TCTAAATTTGCCCTGAGCACCACTCTCTGAGTTCAACTACCATGGCTAGACACCTTTAAC	3480
Q	y	3481	ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT	3540
D	b	3481	ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT	3540
Q	y	3541	CTGGGGCAGTGAGGGGTGGCAGCCAGTGTGGCAGAGAAAAGCACACANGGAAAGAGC	3600
D	b	3541	CTGGGGCAGTGAGGGGTGGCAGCCAGTGTGGCAGAGAAAAGCACACANGGAAAGAGC	3600
Q	y	3601	ACCCAGGACTGTCTATGGAAGAAAAGACAGGACTGCAACTCACCTTTCACAAAAATGAGGA	3660

Db	3601	ACCCAGGACTGCTATATGGAAGAAAGACAGGACTGCAACTCACCCCTTCACAAATGAGGA	3660
Qy	3661	CCAGACACAGCTGATGGTATGAGTTGATGTCAGAGTGCTGGAGCCTCAACATCTGCTCCC	3720
Db	3661	CCAGACACAGCTGATGGTATGAGTTGATGTCAGAGTGCTGGAGCCTCAACATCTGCTCCC	3720
Qy	3721	CTCCTACTACACATGGTTAAGGCCCTGTTGCTCTGCTCCAGGTTACACATCTCTGCACATA	3780
Db	3721	CTCCTACTACACATGGTTAAGGCCCTGTTGCTCTGCTCCAGGTTACACATCTCTGCACATA	3780
Qy	3781	CCTCTTCATGGGTGCCCTCAGACAGGACCTTGGCTTTTCTCTGTTTGAAGCTTTGGGCTA	3840
Db	3781	CCTCTTCATGGGTGCCCTCAGACAGGACCTTGGCTTTTCTCTGTTTGAAGCTTTGGGCTA	3840
Qy	3841	CGTGGATGACACAGCTGTCGTCTTCTATGATNATGAGAGTCGCCGTGTGAGGCCCGAAC	3900
Db	3841	CGTGGATGACACAGCTGTCGTCTTCTATGATCATGAGAGTCGCCGTGTGAGGCCCGAAC	3900
Qy	3901	TCCATGGGTTTCCAGTAPAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	3960
Db	3901	TCCATGGGTTTCCAGTAPAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	3960
Qy	3961	AGGGTGGGATACATGTTTCACTGTTGACTCTCTGAGCTATTAATGGAATAACCAACACAG	4020
Db	3961	AGGGTGGGATACATGTTTCACTGTTGACTCTCTGAGCTATTAATGGAATAACCAACACAG	4020
Qy	4021	CNAGGGTATCTGGAGAGGGGCCCTCACCTTCTCCTGAGGTGTGCACAGCTTTTCATCTTTTC	4080
Db	4021	CNAGGGTATCTGGAGAGGGGCCCTCACCTTCTCCTGAGGTGTGCACAGCTTTTCATCTTTTC	4080
Qy	4081	ATGCATCTTGAAGAAACAGCTGGAAGTCTCGAGGTCCTTGTGGGAGCAGGAAAGAGGSAAG	4140
Db	4081	ATGCATCTTGAAGAAACAGCTGGAAGTCTCGAGGTCCTTGTGGGAGCAGGAAAGAGGSAAG	4140
Qy	4141	GAATTTGCTTCTGAGATCATTTTGGTCTCTTGGGGATGGTGGAAATAGGGACCTATTTCCTT	4200
Db	4141	GAATTTGCTTCTGAGATCATTTTGGTCTCTTGGGGATGGTGGAAATAGGGACCTATTTCCTT	4200
Qy	4201	TGGTTGCAGTTAAACAGGCTGGGGATTTTTCACAGAGTCCACACCCCTGCAGGTCATCCTG	4260
Db	4201	TGGTTGCAGTTAAACAGGCTGGGGATTTTTCACAGAGTCCACACCCCTGCAGGTCATCCTG	4260
Qy	4261	GGCTGGAATGCAAGAAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
Db	4261	GGCTGGAATGCAAGAAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
Qy	4321	CAGGACCACCTTCAATTTCTGCCCTGCACACTGGATTTGGAGAGCAGACAGAACCCAGGGCC	4380
Db	4321	CAGGACCACCTTCAATTTCTGCCCTGNACACTGGATTTGGAGAGCAGACAGAACCCAGGGCC	4380
Qy	4381	TGGCCCCACCAAGCTGGAGTGGGAAAGGCCACAAGATTCCGGGCCAGGCAGAACAGGGCCTAC	4440
Db	4381	TGGCCCCACCAAGCTGGAGTGGGAAAGGCCACAAGATTCCGGGCCAGGCAGAACAGGGCCTAC	4440
Qy	4441	CTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTG	4500
Db	4441	CTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTG	4500
Qy	4501	GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTCTACTCTAGTGGCAGAGTGGAGG	4560
Db	4501	GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTCTACTCTAGTGGCAGAGTGGAGG	4560
Qy	4561	AGGTTGAGGGCACGGNATCCCTTGGTTGAGTTTCAGAGTGGCTGAGGCTGTGTGCCTC	4620
Db	4561	AGGTTGAGGGCACGGNATCCCTTGGTTGAGTTTCAGAGTGGCTGAGGCTGTGTGCCTC	4620
Qy	4621	TCCAAATTTCTGGGAAGGGACTTCTCAATCCCTAGAGTCTCTACCTTATAATTGAGATGTA	4680
Db	4621	TCCAAATTTCTGGGAAGGGACTTCTCAATCCCTAGAGTCTCTACCTTATAATTGAGATGTA	4680
Qy	4681	TGAGACAGCCACAGTCATGGGTTTAAATTTCTTTTCTCCATGCATATGGCTCAAAAGGAA	4740
Db	4681	TGAGACAGCCACAGTCATGGGTTTAAATTTCTTTTCTCCATGCATATGGCTCAAAAGGAA	4740

Qy	4741	GTGTCATAGCGCCCTGCTTTTATTTAATTAACCAATATCTTTTGTATATTTATACCTGTTAA	4800
Db	4741	GTGTCATAGCGCCCTGCTTTTATTTAATTAACCAATATCTTTTGTATATTTATACCTGTTAA	4800
Qy	4801	AAATTCAAGAAATGTCAAGCGCGGGACGGTGCTCACCCCTGTATATCCAGCACTTTGGG	4860
Db	4801	AAATTCAAGAAATGTCAAGCGCGGGACGGTGCTCACCCCTGTATATCCAGCACTTTGGG	4860
Qy	4861	AGGCGGAGCGGGTGTCTCAAAAGTTCAGGAGTTTGTAGACACAGCCTGTACCAACATGTTGAA	4920
Db	4861	AGGCGGAGCGGGTGTCTCAAAAGTTCAGGAGTTTGTAGACACAGCCTGTACCAACATGTTGAA	4920
Qy	4921	ACCCGCTCTCTTAAAAAATACAAAAATTTAGCTGCACAGTCATGCGCACTGTAGTCCCA	4980
Db	4921	ACCCGCTCTCTTAAAAAATACAAAAATTTAGCTGCACAGTCATGCGCACTGTAGTCCCA	4980
Qy	4981	GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTTGGGAAGCGGAAGTTGCACATGA	5040
Db	4981	GCTAATTGGAAGGCTGAGGCAGGAGCATCGCTTGAACCTTGGGAAGCGGAAGTTGCACATGA	5040
Qy	5041	GCCAAAGATCGGGCACTGCACTCCAGCCTTAGGCAGCAGATGAGACTCCCATCTTAAAAAA	5100
Db	5041	GCCAAAGATCGGGCACTGCACTCCAGCCTTAGGCAGCAGATGAGACTCCCATCTTAAAAAA	5100
Qy	5101	AAAAAATAAAAAAAGAGAAATTCAGAGATCTCAGCTATCATATGTAATACAGGACAAA	5160
Db	5101	AAAAAATAAAAAAAGAGAAATTCAGAGATCTCAGCTATCATATGTAATACAGGACAAA	5160
Qy	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCTCTTTAGGTTAAAAAGTTCTTTTCAT	5220
Db	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCTCTTTAGGTTAAAAAGTTCTTTTCAT	5220
Qy	5221	AGAACATAGCAATAATCACATGAAGCTACCTATCTTACAAAGTCGCGTCTCTTATAACAATGC	5280
Db	5221	AGAACATAGCAATAATCACATGAAGCTACCTATCTTACAAAGTCGCGTCTCTTATAACAATGC	5280
Qy	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCATCATTTTCAATGCAACATAA	5340
Db	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCATCATTTTCAATGCAACATAA	5340
Qy	5341	AGGCAATTTTATCTATTCAGAAACAGACATGGGTACAGATATGTATTTACATGTG	5400
Db	5341	AGGCAATTTTATCTATTCAGAAACAGACATGGGTACAGATATGTATTTACATGTG	5400
Qy	5401	AGGAGACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTAGAGTCCAATCTTAGG	5460
Db	5401	AGGAGACAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTAGAGTCCAATCTTAGG	5460
Qy	5461	ACACAAAATGGTGTCCTCTCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTTCCCTTCCTCC	5520
Db	5461	ACACAAAATGGTGTCCTCTCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTTCCCTTCCTCC	5520
Qy	5521	AACCTATAGAAGGAAGTGAAGTTCCAGTCTTCTCGCAAGGTTAAACAGATGCCCTCTC	5580
Db	5521	AACCTATAGAAGGAAGTGAAGTTCCAGTCTTCTCGCAAGGTTAAACAGATGCCCTCTC	5580
Qy	5581	CTCATCTCTCTTCTTCCCTGTCAAGTGCCCTCTTTGGTGAAGGTGACACATCATGTGACC	5640
Db	5581	CTCATCTCTCTTCTTCCCTGTCAAGTGCCCTCTTTGGTGAAGGTGACACATCATGTGACC	5640
Qy	5641	TCCTTCAGTGACCACTCTACCGGTGTGCGGCCCTTGAACCTACTACCCCGAAGCATCACCATG	5700
Db	5641	TCCTTCAGTGACCACTCTACCGGTGTGCGGCCCTTGAACCTACTACCCCGAAGCATCACCATG	5700
Qy	5701	AAGTGGCTGAAGGATAAGCAGCCCAATGGATGCCAAGGAGTTTCSAACCTTAAGACCTATTG	5760
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RESULT 7

US-08-834-497A-5
; Sequence 5, Application US/08834497A
; Patent No. 6140305

GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A

; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 5:
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Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 781 AACTCGGGTTTATTTCCAATGTCACTGTGAGTGTGAGTGTTCCTCCAGTCACTCCAAACAGG 840
Db 781 AACTCGGGTTTATTTCCAATGTCACTGTGAGTGTGAGTGTTCCTCCAGTCACTCCAAACAGG 840
QY 841 AAGTTCTTCCCTGAGTGTGCTCCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900
Db 841 AAGTTCTTCCCTGAGTGTGCTCCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900
QY 901 GGTTCACACTCAGAACGAATGCGTTGGGGGTGGGGCGGGAAGAGTGGGTGGGGA 960
Db 901 GGTTCACACTCAGAACGAATGCGTTGGGGGTGGGGCGGGAAGAGTGGGTGGGGA 960
QY 961 TCTGAATTTCTTCAACCATTTCCACCCACTTTTGGTGAGACTGGGGTGGAGTCTTAGGGT 1020
Db 961 TCTGAATTTCTTCAACCATTTCCACCCACTTTTGGTGAGACTGGGGTGGAGTCTTAGGGT 1020
QY 1021 GGGAGGCTCTTGAGAGGGCTTACCTCGGGCTTTCCCACTCTTGGCAATGTTCTTTT 1080
Db 1021 GGGAGGCTCTTGAGAGGGCTTACCTCGGGCTTTTCCCACTCTTGGCAATGTTCTTTT 1080
QY 1081 CCCTGGAAAAATAGTATATGTTAGTTTGAACGTTTGAACGTTGAACTGAACTTCTCTTCGG 1140
Db 1081 CCCTGGAAAAATAGTATATGTTAGTTTGAACGTTTGAACGTTGAACTGAACTTCTCTTCGG 1140
QY 1141 CTAGGCTTTATTTGCAATGTGCTGTGTAATTAAGAGGCCCTCTCTACAAAGTACTGA 1200
|||||

Db 1141 CTAGGCTTTATTTGCAATGTGCTGTGTAATTAAGAGGCCCTCTCTACAAAGTACTGA 1200
QY 1201 TAAATGAACATGTAGCAATGCACCTCACTTCTTAAGTTACATTATCATATCTGATCTTATTGA 1260
Db 1201 TAAATGAACATGTAGCAATGCACCTCACTTCTTAAGTTACATTATCATATCTGATCTTATTGA 1260
QY 1261 TTTTCACTTAGGCATAGGAGGTAGAGCTAATAATACGTTTATTTTACTAGAACTTAACT 1320
Db 1261 TTTTCACTTAGGCATAGGAGGTAGAGCTAATAATACGTTTATTTTACTAGAACTTAACT 1320
QY 1321 GGAATTCAGATTATATAACTCTTTTCAGGTTTACAAAGAACATAAATAATCTGGTTTTCTG 1380
Db 1321 GGAATTCAGATTATATAACTCTTTTCAGGTTTACAAAGAACATAAATAATCTGGTTTTCTG 1380
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTTAATCTTTAGTTGACAGTGAATTTTCCCTGTAG 1440
Db 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTTAATCTTTAGTTGACAGTGAATTTTCCCTGTAG 1440
QY 1441 TGTAGCACAGTGTCTGTGGTTCACACCGCCCTCAGCACAGCAGCTTTGAGTTTGGTA 1500
Db 1441 TGTAGCACAGTGTCTGTGGTTCACACCGCCCTCAGCACAGCAGCTTTGAGTTTGGTA 1500
QY 1501 CTACGTGTATCCACATTTTACACATGACAAGAAAGAGCATGGCACGGCTTCTCTCTGG 1560
Db 1501 CTACGTGTATCCACATTTTACACATGACAAGAAAGAGCATGGCACGGCTTCTCTCTGG 1560
QY 1561 CAAATTTATTCAGTGTACACTGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
Db 1561 CAAATTTATTCAGTGTACACTGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
QY 1621 TATGATTTCTTAACATCACACTGCAATAGAGTTGAATAAATAATTTTCATGTTGAGCG 1680
Db 1621 TATGATTTCTTAACATCACACTGCAATAGAGTTGAATAAATAATTTTCATGTTGAGCG 1680
QY 1681 AAATATTCATTTTACAAGTGTAAATGAGTCCCAAGCCATGTGTTCGACTGTTCAGGCC 1740
Db 1681 AAATATTCATTTTACAAGTGTAAATGAGTCCCAAGCCATGTGTTCGACTGTTCAGGCC 1740
QY 1741 CAAGGAGAGACGAGGAAACAAAGTCTTTACCTTTGATATTTTGCATTTCTAGTGGGAGA 1800
Db 1741 CAAGGAGAGACGAGGAAACAAAGTCTTTACCTTTGATATTTTGCATTTCTAGTGGGAGA 1800
QY 1801 GATGACAATAACCAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTGGA 1860
Db 1801 GATGACAATAACCAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTGGA 1860
QY 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTGACAGAGACATGAAGGA 1920
Db 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTGACAGAGACATGAAGGA 1920
QY 1921 AATAAGAAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
Db 1921 AATAAGAAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
QY 1981 TTGGATTAAGGAGCGGTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
Db 1981 TTGGATTAAGGAGCGGTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
QY 2041 CGGCTTGGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCTCTGT 2100
Db 2041 CGGCTTGGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCTCTGT 2100
QY 2101 CCTCCCTACTACTAGTGTCTAGGAGCACTCCCGAGTCTTCCAGCAACCAAAATCTCTCT 2160
Db 2101 CCTCCCTACTACTAGTGTCTAGGAGCACTCCCGAGTCTTCCAGCAACCAAAATCTCTCT 2160
QY 2161 AAATTTGGCCACATGTCACCTAGTAGCAAACTCTCTGTTAAGAAAGCTCGGTTGAAAA 2220
Db 2161 AAATTTGGCCACATGTCACCTAGTAGCAAACTCTCTGTTAAGAAAGCTCGGTTGAAAA 2220
QY 2221 AATAAACAAGTGTGTGGGAGTAGAGGCCAAGAGTAGGTAAATGGGCTCAGAAAGAGA 2280
Db 2221 AATAAACAAGTGTGTGGGAGTAGAGGCCAAGAGTAGGTAAATGGGCTCAGAAAGAGA 2280
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QY	2281	GCACAAACAAGTTTGTGCAGGGCCCTGTAGGCTGTGTGTGAATTTAGCCCAAGGAGTA	2340
Db	2281	GCACAAACAAGTTTGTGCAGGGCCCTGTAGGCTGTGTGTGAATTTAGCCCAAGGAGTA	2340
	2281	GCACAAACAAGTTTGTGCAGGGCCCTGTAGGCTGTGTGTGAATTTAGCCCAAGGAGTA	2340
QY	2341	ACAGTGATCTGTACACAGGCTTTTAAAGATTCTCTCTGCTGCTATGTGGAAAGCAGAATG	2400
Db	2341	ACAGTGATCTGTACACAGGCTTTTAAAGATTCTCTCTGCTGCTATGTGGAAAGCAGAATG	2400
	2341	ACAGTGATCTGTACACAGGCTTTTAAAGATTCTCTCTGCTGCTATGTGGAAAGCAGAATG	2400
QY	2401	AAGGAGCAACAGTATAAAGCAGGAGCCACGACGAAGAGCTGTACACAGTCCACGCAAG	2460
Db	2401	AAGGAGCAACAGTATAAAGCAGGAGCCACGACGAAGAGCTGTACACAGTCCACGCAAG	2460
	2401	AAGGAGCAACAGTATAAAGCAGGAGCCACGACGAAGAGCTGTACACAGTCCACGCAAG	2460
QY	2461	AGGTACTGGAGTGGGCTGGGTGGGACAGAAAGGGAGTGACAAACATTTGTCCTCTGAA	2520
Db	2461	AGGTACTGGAGTGGGCTGGGTGGGACAGAAAGGGAGTGACAAACATTTGTCCTCTGAA	2520
	2461	AGGTACTGGAGTGGGCTGGGTGGGACAGAAAGGGAGTGACAAACATTTGTCCTCTGAA	2520
QY	2521	TATATTCTGAAGGAAGCTTGCTGAAGGATTCTATGTGTGTGAGAGAAGAAGAATTGG	2580
Db	2521	TATATTCTGAAGGAAGCTTGCTGAAGGATTCTATGTGTGTGAGAGAAGAAGAATTGG	2580
	2521	TATATTCTGAAGGAAGCTTGCTGAAGGATTCTATGTGTGTGAGAGAAGAAGAATTGG	2580
QY	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA	2640
Db	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA	2640
	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA	2640
QY	2641	GTTCAAGACCAGCTCGGCAACACACAGCAAAACCCCTCTCTACAAAAATACAAAAATTA	2700
Db	2641	GTTCAAGACCAGCTCGGCAACACACAGCAAAACCCCTCTCTACAAAAATACAAAAATTA	2700
	2641	GTTCAAGACCAGCTCGGCAACACACAGCAAAACCCCTCTCTACAAAAATACAAAAATTA	2700
QY	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGA	2760
Db	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGA	2760
	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGGA	2760
QY	2761	TTGCTTGAGCCCAAGGAAGTTGAGGTGCGAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820
Db	2761	TTGCTTGAGCCCAAGGAAGTTGAGGTGCGAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820
	2761	TTGCTTGAGCCCAAGGAAGTTGAGGTGCGAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820
QY	2821	CTAGGTGACAGAGCAAGACCCCTGTCTCCCTGTACCCCTGAAACGAGAGAGTAAAGT	2880
Db	2821	CTAGGTGACAGAGCAAGACCCCTGTCTCCCTGTACCCCTGAAACGAGAGAGTAAAGT	2880
	2821	CTAGGTGACAGAGCAAGACCCCTGTCTCCCTGTACCCCTGAAACGAGAGAGTAAAGT	2880
QY	2881	TGACTTTGTCTTTATTTTAAATTTTATTGGCTCAGCAGTGGGCTAAATTTGGCAATGCCAT	2940
Db	2881	TGACTTTGTCTTTATTTTAAATTTTATTGGCTCAGCAGTGGGCTAAATTTGGCAATGCCAT	2940
	2881	TGACTTTGTCTTTATTTTAAATTTTATTGGCTCAGCAGTGGGCTAAATTTGGCAATGCCAT	2940
QY	2941	TTCTGAGATGGTGAGGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGGATTCGCAATTG	3000
Db	2941	TTCTGAGATGGTGAGGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGGATTCGCAATTG	3000
	2941	TTCTGAGATGGTGAGGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGGATTCGCAATTG	3000
QY	3001	GGACATGTTAAGTTTTCAGATTCACAGTCAAGCTTCCAAGTGTGAGGCCACATAGGCAGTT	3060
Db	3001	GGACATGTTAAGTTTTCAGATTCACAGTCAAGCTTCCAAGTGTGAGGCCACATAGGCAGTT	3060
	3001	GGACATGTTAAGTTTTCAGATTCACAGTCAAGCTTCCAAGTGTGAGGCCACATAGGCAGTT	3060
QY	3061	CAGTGTAGAATTCAGGACCAAGGCTGGGCACGGTGGCTACTTCTGTAATCCGAGCACT	3120
Db	3061	CAGTGTAGAATTCAGGACCAAGGCTGGGCACGGTGGCTACTTCTGTAATCCGAGCACT	3120
	3061	CAGTGTAGAATTCAGGACCAAGGCTGGGCACGGTGGCTACTTCTGTAATCCGAGCACT	3120
QY	3121	TTGGTGGCTGAGGCAGGTAGATCAATTTGAGTCAAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
Db	3121	TTGGTGGCTGAGGCAGGTAGATCAATTTGAGTCAAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
	3121	TTGGTGGCTGAGGCAGGTAGATCAATTTGAGTCAAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
QY	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTAGCCCTGGTGTGGTGGCCACGCCT	3240
Db	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTAGCCCTGGTGTGGTGGCCACGCCT	3240
	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTAGCCCTGGTGTGGTGGCCACGCCT	3240
QY	3241	ATAGTCCCAGGTTTTCAGGAGGCTTTAGTGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
Db	3241	ATAGTCCCAGGTTTTCAGGAGGCTTTAGTGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
	3241	ATAGTCCCAGGTTTTCAGGAGGCTTTAGTGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
QY	3301	TTGCAGTGAGCTGAGATTTGCCACTGCACCTGCAGCTGGGTGTATGAGGTGAGACTCTGT	3360
Db	3301	TTGCAGTGAGCTGAGATTTGCCACTGCACCTGCAGCTGGGTGTATGAGGTGAGACTCTGT	3360
	3301	TTGCAGTGAGCTGAGATTTGCCACTGCACCTGCAGCTGGGTGTATGAGGTGAGACTCTGT	3360

QY	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATATTCTCTCAGGATTTGGG	3420
DB	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAATATTCTCTCAGGATTTGGG	3420
QY	3421	TCTAATTTGGCCTGAGCACCACACTCCTGAGTTCACTACCATGGCTAGACACACCTTAAC	3480
DB	3421	TCTAATTTGGCCTGAGCACCACACTCCTGAGTTCACTACCATGGCTAGACACACCTTAAC	3480
QY	3481	ATTTTCTAGAAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT	3540
DB	3481	ATTTTCTAGAAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT	3540
QY	3541	CTGGGGCAGTGAAGGGGTGGCAGCCACGTGTGGCAGAGAAAAGCACAAAGGAAGAGC	3600
DB	3541	CTGGGGCAGTGAAGGGGTGGCAGCCACGTGTGGCAGAGAAAAGCACAAAGGAAGAGC	3600
QY	3601	ACCAGGACTGTCTATATGGAAGAAAGACAGGACTGCACTCACCCCTTCACAAATAGGA	3660
DB	3601	ACCAGGACTGTCTATATGGAAGAAAGACAGGACTGCACTCACCCCTTCACAAATAGGA	3660
QY	3661	CCAGACAGCTGATGTATGAGTTGATGCAAGTGTGTGGAGCCTCAACATCCTGCTCCC	3720
DB	3661	CCAGACAGCTGATGTATGAGTTGATGCAAGTGTGTGGAGCCTCAACATCCTGCTCCC	3720
QY	3721	CTCTACTACACATGGTTAAGGCGCTGTGCTCTGTCTCCAGTTCCACACTCTCTGCACTA	3780
DB	3721	CTCTACTACACATGGTTAAGGCGCTGTGCTCTGTCTCCAGTTTCACACTCTCTGCACTA	3780
QY	3781	CCTCTCATGGTGCCCTCAGACAGCAGCCTTGGTCTTTTCTTGTGTAAGCTTTGGGCTA	3840
DB	3781	CCTCTCATGGTGCCCTCAGACAGCAGCCTTGGTCTTTTCTTGTGTAAGCTTTGGGCTA	3840
QY	3841	CGTGGATGACCAGCTGTCCGTCTTCTATGATNATGAGAGTCCCGTGTGGAGCCCGGAAC	3900
DB	3841	CGTGGATGACCAGCTGTCCGTCTTCTATGATNATGAGAGTCCCGTGTGGAGCCCGGAAC	3900
QY	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGTCAGTCTGAGTCTGAA	3960
DB	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGTCAGTCTGAGTCTGAA	3960
QY	3961	AGGCTGGATCACATGTTCACTGTTGACATCTGGACTATTATGGAATATCACACCACAG	4020
DB	3961	AGGCTGGATCACATGTTCACTGTTGACATCTGGACTATTATGGAATATCACACCACAG	4020
QY	4021	CAAGGGTATGTGGAGAGGGGCCCTACCTTCCTGAGTGTGTCAGAGCTTTTCATCTTTTC	4080
DB	4021	CAAGGGTATGTGGAGAGGGGCCCTACCTTCCTGAGTGTGTCAGAGCTTTTCATCTTTTC	4080
QY	4081	ATGCATCTTGAAGAAACAGCTGGAAAGTCTGAGGCTTGTGGAGCAGGGAAGGGAAG	4140
DB	4081	ATGCATCTTGAAGAAACAGCTGGAAAGTCTGAGGCTTGTGGAGCAGGGAAGGGAAG	4140
QY	4141	GAATTTGCTTCCCTGAGATCATTTGGTCCCTTGGGGATGGTGGAAATAGGACCTATTCCCT	4200
DB	4141	GAATTTGCTTCCCTGAGATCATTTGGTCCCTTGGGGATGGTGGAAATAGGACCTATTCCCT	4200
QY	4201	TGGTTGCAGTTAAACAGGCTGGGGATTTTTCACAGAGTCCACACCCCTCAGGTCATCTGT	4260
DB	4201	TGGTTGCAGTTAAACAGGCTGGGGATTTTTCACAGAGTCCACACCCCTCAGGTCATCTGT	4260
QY	4261	GGCTGTGAATGCAAGAAGACAACTACCGAGGCTACTGGAAGTACGGGTATGATGGG	4320
DB	4261	GGCTGTGAATGCAAGAAGACAACTACCGAGGCTACTGGAAGTACGGGTATGATGGG	4320
QY	4321	CAGACACACCTTGAAATCTGCCCTGACACACTGGATTGGAGAGCAGCAACCCAGGGCC	4380
DB	4321	CAGACACACCTTGAAATCTGCCCTGACACACTGGATTGGAGAGCAGCAACCCAGGGCC	4380
QY	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCACAGATTCCGGCCAGCCAGCAACAGGCGCTAC	4440
DB	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCACAGATTCCGGCCAGCCAGCAACAGGCGCTAC	4440
QY	4441	CTGAGAGGAGCTGCGCCTGCACAGCTGCACAGCTTGTCTGGAGCTGGGAGAGTGTTTTG	4500

Db	4441		CTGAGAGGAC	TGCCTGCACAGCTGCACAGTTCCTGAGCTCGGGAGAGTGTTTC		4500
Qy	4501	GACCAACAAGT	ATGTTGGAACACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560		
Db	4501	GACCAACAAGT	ATGTTGGAACACACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560		
Qy	4561	AGTTGCAGGCACGGA	ATCCCTGGTTGGAGTTTTCAGAGTGGCTGAGGCTGTGTGCCTC	4620		
Db	4561	AGTTGCAGGCACGGA	ATCCCTGGTTGGAGTTTTCAGAGTGGCTGAGGCTGTGTGCCTC	4620		
Qy	4621	TCCAAATCTCTGGA	AGGGACTTTCCTCAATCCCTAGAGTCTACCTTATAATTCAGATGTA	4680		
Db	4621	TCCAAATCTCTGGA	AGGGACTTTCCTCAATCCCTAGAGTCTACCTTATAATTCAGATGTA	4680		
Qy	4681	TGAGACAGCCACAAG	TCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA	4740		
Db	4681	TGAGACAGCCACAAG	TCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA	4740		
Qy	4741	GTGTCTATGGCCCT	TGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA	4800		
Db	4741	GTGTCTATGGCCCT	TGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA	4800		
Qy	4801	AAATTCAGAAAT	GTCAAGGCGGGCACAGGTGACCTGATCCCTGTATATCCACGACATTTGGG	4860		
Db	4801	AAATTCAGAAAT	GTCAAGGCGGGCACAGGTGACCTGATCCCTGTATATCCACGACATTTGGG	4860		
Qy	4861	AGGCCGAGGCGGT	GTCAACAGGTCAGAGTTTCAGACACAGCTGACCAACATGTTGAA	4920		
Db	4861	AGGCCGAGGCGGT	GTCAACAGGTCAGAGTTTCAGACACAGCTGACCAACATGTTGAA	4920		
Qy	4921	ACCCGTCCTCTAAA	AAAAATACAAAATTAGCTGGTCACAGTCAATGCGACCTGTAGTCCCA	4980		
Db	4921	ACCCGTCCTCTAAA	AAAAATACAAAATTAGCTGGTCACAGTCAATGCGACCTGTAGTCCCA	4980		
Qy	4981	GCTAATTTGGAAG	CGCTGAGGACGAGCATCGCTTGAACCTGGGAAGCGGAAGTTCACATGA	5040		
Db	4981	GCTAATTTGGAAG	CGCTGAGGACGAGCATCGCTTGAACCTGGGAAGCGGAAGTTCACATGA	5040		
Qy	5041	GCCAAGATCGGCC	CTGCACCTCCAGCTPAGCCAGCAGTGAGACTCCATCTTTAAAAA	5100		
Db	5041	GCCAAGATCGGCC	CTGCACCTCCAGCTPAGCCAGCAGTGAGACTCCATCTTTAAAAA	5100		
Qy	5101	AAAAA	AAAAAAGAAATTCAGAGATCTCAGCTATCATATGAATACAGACAAA	5160		
Db	5101	AAAAA	AAAAAAGAAATTCAGAGATCTCAGCTATCATATGAATACAGACAAA	5160		
Qy	5161	ATATCAAGT	GAGGCACCTATCAGAGTAGAAGATCCTTTAGGTTAAAAGTTCTTCAT	5220		
Db	5161	ATATCAAGT	GAGGCACCTATCAGAGTAGAAGATCCTTTAGGTTAAAAGTTCTTCAT	5220		
Qy	5221	AGACATAGCA	TAATCACTGANGCTACCTATCTACAGTCCGCTCTTATACATGC	5280		
Db	5221	AGACATAGCA	TAATCACTGANGCTACCTATCTACAGTCCGCTCTTATACATGC	5280		
Qy	5281	CTCCTAGGTT	GACCCAGGTGAAACTGACCATCTGTATTCAATCATTTCAATGCACATAA	5340		
Db	5281	CTCCTAGGTT	GACCCAGGTGAAACTGACCATCTGTATTCAATCATTTCAATGCACATAA	5340		
Qy	5341	AGGCAATTTTAT	CTATCAGAACAAAGAACATGGGTAAACAGATATGTATATTACATGTG	5400		
Db	5341	AGGCAATTTTAT	CTATCAGAACAAAGAACATGGGTAAACAGATATGTATATTACATGTG	5400		
Qy	5401	AGGAGACAGCT	GATCTGACTGCTCTCCAAGTGACACTGTGTAGAGTCCAATCTTAGG	5460		
Db	5401	AGGAGACAGCT	GATCTGACTGCTCTCCAAGTGACACTGTGTAGAGTCCAATCTTAGG	5460		
Qy	5461	ACACAAATGGT	CTCTCCTGTAGCTTTTCTGAAAAGGGTATTTCCCTTCCTCC	5520		
Db	5461	ACACAAATGGT	CTCTCCTGTAGCTTTTCTGAAAAGGGTATTTCCCTTCCTCC	5520		
Qy	5521	AACCTATAGA	AGGAAGTGAAGTTCAGTCTTCCTGGCAAGGGTAAACAGATCCCTCTC	5580		

Db	5521	AACCTATAGAAAGGATGAAGGTTCCAGTCTCTTCCTGGCAAGGGTAAACAGATCCCCCTCTC	5580
Qy	5581	CTCATCCTTCCCTCTTTCCTCTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC	5640
Db	5581	CTCATCCTTCCCTCTTTCCTCTCAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACC	5640
Qy	5641	TCCTCAGTGACCACTCTACGGGTGTCGGGCTTTGAACCTACTACCCCCAGAACATCACCANTG	5700
Db	5641	TCCTCAGTGACCACTCTACGGGTGTCGGGCTTTGAACCTACTACCCCCAGAACATCACCANTG	5700
Qy	5701	AAGTGGCTGAAGGATRAGCAGCCAATGGATGCCAAGGAGTTCGAACCTTAAGACAGTATTG	5760
Db	5701	AAGTGGCTGAAGGATRAGCAGCCAATGGATGCCAAGGAGTTCGAACCTTAAGACAGTATTG	5760
Qy	5761	CCCAATGGGATGGGACCTACCAAGGCTCGATAACTCTGGCTGTACCCCTCGGGGAAGAG	5820
Db	5761	CCCAATGGGATGGGACCTACCAAGGCTCGATAACTCTGGCTGTACCCCTCGGGGAAGAG	5820
Qy	5821	CAGAGATATACGTNCCAGSTGGAGCACCCAGGCCCTGGATCAGCCCCCTCATTTGTGATCTGG	5880
Db	5821	CAGAGATATACGTNCCAGSTGGAGCACCCAGGCCCTGGATCAGCCCCCTCATTTGTGATCTGG	5880
Qy	5881	GGTATGTACTGATGAGAGCCAGGAGCTCAGAAAATCTATTGGGGGGTTGAGAGAGTGCC	5940
Db	5881	GGTATGTACTGATGAGAGCCAGGAGCTCAGAAAATCTATTGGGGGGTTGAGAGAGTGCC	5940
Qy	5941	TGAGGAGTAAATTATGSCAGTGAGATGAGGATCTGCTCTTTGTAGGGGGTTGGGCTGAGG	6000
Db	5941	TGAGGAGTAAATTATGSCAGTGAGATGAGGATCTGCTCTTTGTAGGGGGTTGGGCTGAGG	6000
Qy	6001	GTGCAATCAAAAGCCTTAACTTGTCTTTTCTGTCTTTTAGAGCCCCCTACCGTCTGGCACCC	6060
Db	6001	GTGCAATCAAAAGCCTTAACTTGTCTTTTCTGTCTTTTAGAGCCCCCTACCGTCTGGCACCC	6060
Qy	6061	TAGTCATGTGAGTCATCAGTGGAAATGCTGTTTTTGTCTCGTCACTTTGTTCATTGGGAATTT	6120
Db	6061	TAGTCATGTGAGTCATCAGTGGAAATGCTGTTTTTGTCTCGTCACTTTGTTCATTGGGAATTT	6120
Qy	6121	TGTTTCATAATATTAAAGGAAGAGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT	6180
Db	6121	TGTTTCATAATATTAAAGGAAGAGCAGGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT	6180
Qy	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	6240
Db	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	6240
Qy	6241	AAGCATTTTTCTCATTTATATTCTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAT	6300
Db	6241	AAGCATTTTTCTCATTTATATTCTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAT	6300
Qy	6301	AATGGTTCTCCCGAATGAAAGTCTCAATTCAACAAACATCTTCAGAGCACCTACTAT	6360
Db	6301	AATGGTTCTCCCGAATGAAAGTCTCAATTCAACAAACATCTTCAGAGCACCTACTAT	6360
Qy	6361	TTTGCAAGAGCTGTTAAGGTAGTACAGGGGCTTTGAGTTTGAGAAGTCACTGTGGCTAT	6420
Db	6361	TTTGCAAGAGCTGTTAAGGTAGTACAGGGGCTTTGAGTTTGAGAAGTCACTGTGGCTAT	6420
Qy	6421	TCTCAGAACCCCAATCTGTTAGGGAATGAATTTGATAGCAAGTAAATGTAGTTAAAGAAG	6480
Db	6421	TCTCAGAACCCCAATCTGTTAGGGAATGAATTTGATAGCAAGTAAATGTAGTTAAAGAAG	6480
Qy	6481	ACCCCATGAGTCTCTAAAGCAGCAGGAAGCAAAATGCTTAGGGTGTCAAAGGAAAGAATG	6540
Db	6481	ACCCCATGAGTCTCTAAAGCAGCAGGAAGCAAAATGCTTAGGGTGTCAAAGGAAAGAATG	6540
Qy	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAGCTTGGATTCCA	6600
Db	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAGCTTGGATTCCA	6600
Qy	6601	TTAGGTGAGGTTGAAGATGATGGAGGCTCTACACAGCAGGACCAACCATGCCAAGTAGGA	6660
Db	6601	TTAGGTGAGGTTGAAGATGATGGAGGCTCTACACAGCAGGACCAACCATGCCAAGTAGGA	6660

QY 6661 GAGTAAAGGCATCTGGGAGATTAGAAATAATTACTGTACCTTAACCCCTGAGTTTCGGT 6720
DB |||||||
QY 6661 GAGTAAAGGCATCTGGGAGATTAGAAATAATTACTGTACCTTAACCCCTGAGTTTCGGT 6720
DB |||||||
QY 6721 AGCTATCACTACCAAAATATGCAATTTCTACCCCTGAACACACTCTGTGTAGGGAAGA 6780
DB |||||||
QY 6721 AGCTATCACTACCAAAATATGCAATTTCTACCCCTGAACACACTCTGTGTAGGGAAGA 6780
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RESULT 8

US-08-834-497A-7
; Sequence 7, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnikke, Andreas
; APPLICANT: Ruddy, David

APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 7:
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US-08-834-497A-7

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QY 3841 CGTGGATGACCAAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCGCAAC 3900
Db 3841 CGTGGATGACCAAGCTGTTCGTGTTCTATGATGATGAGAGTCGCCGTGTGGAGCCCGCAAC 3900
QY 3901 TCCATGGCTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGTCTGAA 3960
Db 3901 TCCATGGCTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGTCTGAA 3960
QY 3961 AGGGTGGGATCACATGTTTCACTGTGACTTCTGGACTATTATGAAAAATCACACACCAG 4020
Db 3961 AGGGTGGGATCACATGTTTCACTGTGACTTCTGGACTATTATGAAAAATCACACACCAG 4020
QY 4021 CAAAGGATGTGGAGAGGGGCCCTCACCTTCCTGAGGTGTGCAGAGCTTTTCATCTTTTC 4080
|||||

Db 4021 CAAAGGATGTGGAGAGGGGCCCTCACCTTCCTGAGGTGTGTCAGAGCTTTTCATCTTTTC 4080
QY 4081 ATGCATCTTGAAGAAACACAGCTGGAAGTCTGAGGCTCTGTGGAGCAGGAAAGAGGAAG 4140
Db 4081 ATGCATCTTGAAGAAACACAGCTGGAAGTCTGAGGCTCTGTGGAGCAGGAAAGAGGAAG 4140
QY 4141 GAATTTGCTTCCCTGAGATCATTTTGGTCTTGGGATGGTGAATAAGGACCTTATTCCTT 4200
Db 4141 GAATTTGCTTCCCTGAGATCATTTTGGTCTTGGGATGGTGAATAAGGACCTTATTCCTT 4200
QY 4201 TGGTTCAGTAAACAAGGCTGGGATTTTTCAGAGTCCACACACCTTCAGGTCATCTCTG 4260
Db 4201 TGGTTCAGTAAACAAGGCTGGGATTTTTCAGAGTCCACACACCTTCAGGTCATCTCTG 4260
QY 4261 GGCCTGCAAAATGCAAGNAGAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 4320
Db 4261 GGCCTGCAAAATGCAAGNAGAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 4320
QY 4321 CAGGACCACCTTCAATTTCTGCCCTGCACACTGGATTGGAGAGCAGACAACCCAGGGCC 4380
Db 4321 CAGGACCACCTTCAATTTCTGCCCTGCACACTGGATTGGAGAGCAGACAACCCAGGGCC 4380
QY 4381 TGGCCCAACCAAGCTGGAGTGGGAAAGCACAAGATTCGGGCCAGGACAGAGGGCCTAC 4440
Db 4381 TGGCCCAACCAAGCTGGAGTGGGAAAGCACAAGATTCGGGCCAGGACAGAGGGCCTAC 4440
QY 4441 CTGGAGGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTTGAGGCTGGGGAGAGGTGTTTG 4500
Db 4441 CTGGAGGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTTGAGGCTGGGGAGAGGTGTTTG 4500
QY 4501 GACCAACAAGGTATGTTGGAACACACTTCTGCCCTATCTCTAGTGCAGAGTGGAGG 4560
Db 4501 GACCAACAAGGTATGTTGGAACACACTTCTGCCCTATCTCTAGTGCAGAGTGGAGG 4560
QY 4561 AGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTCCTC 4620
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QY 4621 TCCAAATTCGGAAGGAGGACTTCTCAATCCTAGAGTCTCTACCTTATATTCAGATGTA 4680
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QY 4681 TGACAGCCACCAAGTCAATGCTGGTTTAAATTTCTTCCATGCATATGCTCAAGGGAA 4740
Db 4681 TGACAGCCACCAAGTCAATGCTGGTTTAAATTTCTTCCATGCATATGCTCAAGGGAA 4740
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Qy	5161	ATATCAAGTGAGCCACTTATCAGAGTAGAAGAAATCCTTTTAGGTTAAAGATTTCTTTTCAT	5222
Db	5161	ATATCAAGTGAGCCACTTATCAGAGTAGAAGAAATCCTTTTAGGTTAAAGATTTCTTTTCAT	5220
Qy	5221	AGACATAGCAATAATACACTGAAGCTACCTATCTTACAAGTCCCGTCTTTATACAAATGC	5280
Db	5221	AGACATAGCAATAATACACTGAAGCTACCTATCTTACAAGTCCCGTCTTTATACAAATGC	5280
Qy	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA	5340
Db	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA	5340
Qy	5341	AGGCAATTTTATCTATCAGAACAAAGAACATGGGTAAACAGATATGATATTTACATGTG	5400
Db	5341	AGGCAATTTTATCTATCAGAACAAAGAACATGGGTAAACAGATATGATATTTACATGTG	5400
Qy	5401	AGGAGACAGCTGATCTACCTGCTCTCCAAGTGACACTGTTTAGAGTCCCAATCTTAGG	5460
Db	5401	AGGAGAACAGCTGATCTGACTGCTCTCCAAGTGACACTGTTTAGAGTCCCAATCTTAGG	5460
Qy	5461	ACACAAATGGTCTCTCCTCTAGCTTGTTTTTTCTCGAAAAGGGTATTTCTCTCTCC	5520
Db	5461	ACACAAATGGTCTCTCCTCTAGCTTGTTTTTTCTCGAAAAGGGTATTTCTCTCTCC	5520
Qy	5521	AACCTATAGAAGAGTGAAAGTTCCAGTCTTCTTCGGCAAGGGTAAACAGATCCCCTCTC	5580
Db	5521	AACCTATAGAAGAGTGAAAGTTCCAGTCTTCTTCGGCAAGGGTAAACAGATCCCCTCTC	5580
Qy	5581	CTCATCTCTCCTCTTCTCTGCTCAAGTGCTCCTTTGGTGAAGGTGACACATCATGTGACC	5640
Db	5581	CTCATCTCTCCTCTTCTCTGCTCAAGTGCTCCTTTGGTGAAGGTGACACATCATGTGACC	5640
Qy	5641	TCCTTCAGTGACCCTCTACGGTGTGCGGCTTTGAACTACTACCCCCAGAACATCACCCTG	5700
Db	5641	TCCTTCAGTGACCCTCTACGGTGTGCGGCTTTGAACTACTACCCCCAGAACATCACCCTG	5700
Qy	5701	AAGTGGCTGAAGGATTAAGCAGCAATGGATGCCAAGGAGTTGGAACCTAAGACGTTATTG	5760
Db	5701	AAGTGGCTGAAGGATTAAGCAGCAATGGATGCCAAGGAGTTGGAACCTAAGACGTTATTG	5760
Qy	5761	CCCAATGGGATGGGACCTTACCAGGCTTGATTAACCTTTGGCTGTACCCCTGGGGAAGAG	5820
Db	5761	CCCAATGGGATGGGACCTTACCAGGCTTGATTAACCTTTGGCTGTACCCCTGGGGAAGAG	5820
Qy	5821	CAGAGATATACGTNCCAGGTGGAGCACCCAGGCTTGGATCAGCCCTCATTTGTGATCTGG	5880
Db	5821	CAGAGATATACGTNCCAGGTGGAGCACCCAGGCTTGGATCAGCCCTCATTTGTGATCTGG	5880
Qy	5881	GGTATGTACTGATGAGCCAGGAGCTCAGAAAATCTATTGGGGGTGAGAGAGTGCC	5940
Db	5881	GGTATGTACTGATGAGCCAGGAGCTCAGAAAATCTATTGGGGGTGAGAGAGTGCC	5940
Qy	5941	TGAGGAGTAAATTATGGCAGTGAGATGAGGATCTCTCTTTGTTAGGGGGTGGGCTGAGG	6000
Db	5941	TGAGGAGTAAATTATGGCAGTGAGATGAGGATCTCTCTTTGTTAGGGGGTGGGCTGAGG	6000
Qy	6001	GTGGCAATCAAGGCTTTTAACTTTCCTTTTTCGTTTTTAGGCCCTCACGCTCTGGCACCC	6060
Db	6001	GTGGCAATCAAGGCTTTTAACTTTCCTTTTTCGTTTTTAGGCCCTCACGCTCTGGCACCC	6060
Qy	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTTCGTCATCTGTTCATTTGGAAATTT	6120
Db	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTTCGTCATCTGTTCATTTGGAAATTT	6120
Qy	6121	TGTTTCATAAATTAAGGAAGAGCGGGTTCAAGTGAGTAGGAACAAAGGGGGAAGTCTCT	6180
Db	6121	TGTTTCATAAATTAAGGAAGAGCGGGTTCAAGTGAGTAGGAACAAAGGGGGAAGTCTCT	6180
Qy	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	6240
Db	6181	TAGTACCTCTGCCCCAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	6240

Qy	6241	AAGCATTTTCTCATTTATATCTTTGGGGACACAGCAGCTCCCTGGGACAGAAAAAT	6300
Db	6241	AAGCATTTTCTCATTTATATCTTTGGGGACACAGCAGCTCCCTGGGACAGAAAAAT	6300
Qy	6301	AATGTTTCTCCCGAAGTAAAGTCTCTAATTTCAACAACAATCTTTCAGAGCACCTACTAT	6360
Db	6301	AATGTTTCTCCCGAAGTAAAGTCTCTAATTTCAACAACAATCTTTCAGAGCACCTACTAT	6360
Qy	6361	TTTCAAGAGCTGTTTAAAGTAGTACAGGGGCTTTTGGGTTGAGAAGTCACTGTGGCTAT	6420
Db	6361	TTTCAAGAGCTGTTTAAAGTAGTACAGGGGCTTTTGGGTTGAGAAGTCACTGTGGCTAT	6420
Qy	6421	TCTCAGAACCCAAATCTGTTAGGAATGAATTGATACCAAGTAAATCTAGTTAAAGAG	6480
Db	6421	TCTCAGAACCCAAATCTGTTAGGAATGAATTGATACCAAGTAAATCTAGTTAAAGAG	6480
Qy	6481	ACCCATAGAGTCTCTAAAGCAGCAGGAAGCAAAATGCTTTAGGGTGTCAAAGGAAAGAAATG	6540
Db	6481	ACCCATAGAGTCTCTAAAGCAGCAGGAAGCAAAATGCTTTAGGGTGTCAAAGGAAAGAAATG	6540
Qy	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAGCTGGATTCCA	6600
Db	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAGCTGGATTCCA	6600
Qy	6601	TTAGGTGAGGTTGAAGATGATGGAGGCTCTACACAGCGGAGCAACCATGCCAAGTAGGA	6660
Db	6601	TTAGGTGAGGTTGAAGATGATGGAGGCTCTACACAGCGGAGCAACCATGCCAAGTAGGA	6660
Qy	6661	GAGTATAAGGCATCTCTGGGAGATTGAATAATTAATCTGTACCTTAAACCCTGAGTTTCCGT	6720
Db	6661	GAGTATAAGGCATCTCTGGGAGATTGAATAATTAATCTGTACCTTAAACCCTGAGTTTCCGT	6720
Qy	6721	AGCTATCACTCACCAATTATGCAATTTCTACCCCTTGAACATCTGTGTTGAGGAAAAGA	6780
Db	6721	AGCTATCACTCACCAATTATGCAATTTCTACCCCTTGAACATCTGTGTTGAGGAAAAGA	6780
Qy	6781	GAATCAGAAAAGCCAGCTCATACAGAGTCCAAGSGTCTTTTGGGATATTGGGTTATGA	6840
Db	6781	GAATCAGAAAAGCCAGCTCATACAGAGTCCAAGSGTCTTTTGGGATATTGGGTTATGA	6840
Qy	6841	TCAGTGGGTGTCATTCAAGGATCCTTAAGAAAGGAGGCCAGGATCCCTTATATGGT	6900
Db	6841	TCAGTGGGTGTCATTCAAGGATCCTTAAGAAAGGAGGCCAGGATCCCTTATATGGT	6900
Qy	6901	AATGTGTTGTTAAGAGATTAGATGAGAGGTGAGAGACCCAGTTAGAAAGCCCAATAAGCAT	6960
Db	6901	AATGTGTTGTTAAGAGATTAGATGAGAGGTGAGAGACCCAGTTAGAAAGCCCAATAAGCAT	6960
Qy	6961	TTCAGATGAGAGATAATGGTCTTCAAATCCAATAGTGCCAGCTCTAAATTGAGATGG	7020
Db	6961	TTCAGATGAGAGATAATGGTCTTCAAATCCAATAGTGCCAGCTCTAAATTGAGATGG	7020
Qy	7021	GTGAATGAGGAAAATAGGAAGAGAGAAGCAGGCAAGATGGTGCTTGTGTATGCGCT	7080
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Db	7081	CTTTCCTGGGTCTCTGTCCTCAAATCCAATAGTGCCAGCTCTAAATTGAGATGG	7140
Qy	7141	TGAGTGACGCGCCCTGCAGACTCACTGTGGGAGGAGACAAAACTAGAGACTCAAGA	7200
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Qy	7201	GGGAGTGCATTTATGAGCTCTTCAATGTTTTCAGSAGAGAGTTGAACCTAAACATAGAAAT	7260
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Qy	7321	TTAGGTTTCTGAGTTCTCGATGCCGCTGATCCTAGCTGTCAGCTCTCCCTCGGAAGCTG	7380

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Db 10801 TAAATCCCCCAATTTTTCATAAAC 10825
RESULT 9
US-09-503-444A-1
: Sequence 1, Application US/09503444A
: Patent No. 6228594
: GENERAL INFORMATION:
: APPLICANT: Thomas, Winston J.
: APPLICANT: Drayna, Dennis T.
: APPLICANT: Feder, John N.
: APPLICANT: Gnirke, Andreas
: APPLICANT: Ruddy, David
: APPLICANT: Tsuchihashi, Zenta
: APPLICANT: Wolff, Roger K.
: TITLE OF INVENTION: Hereditary Hemochromatosis Gene
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: WordPerfect Version 8
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/503,444A
: FILING DATE: 14-Feb-2000
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/652,265
: FILING DATE: 23-May-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/632,673
: FILING DATE: 16-Apr-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/630,912
: FILING DATE: 04-Apr-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 8907-0088-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-790-9090
: TELEFAX: 212-869-9741
: TELEX: 66141
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10825 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS

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; Patent No. 6328594
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; GENERAL INFORMATION:
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; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
;
; TITLE OF INVENTION: Hereditary H
;
; NUMBER OF SEQUENCES: 44
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Pennie & Edmonds LL
;
; STREET: 1155 Avenue of the Ame
;
; CITY: New York
;
; STATE: New York
;
; COUNTRY: USA
;
; ZIP: 10036
;
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: Windows 95
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; SOFTWARE: Wordperfect Version
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> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/09/503.444A
> FILING DATE: 14-Feb-2000
> CLASSIFICATION:
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: 08/652,265
> FILING DATE: 23-May-1996
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: 08/632,673
> FILING DATE: 16-Apr-1996
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: 08/630,912
> FILING DATE: 04-Apr-1996
> ATTORNEY/AGENT INFORMATION:
> NAME: Poissant, Brian M.
> REGISTRATION NUMBER: 28,462
> REFERENCE/DOCKET NUMBER: 8907-0088-999
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 212-790-9090
> TELEFAX: 212-869-3741
> TELEX: 66141
> INFORMATION FOR SEQ ID NO: 3:
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> US-09-503-444A-3
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Db 121 TCAGGATTTAAACCAAGGGGACACTGGATCACTAGTGTTCACAAGCAGGTACCTT 180
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTCTAAAGACCTGTGTCTTTTCCACAGCAAGTT 240
Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGNAAGACCTGTGTCTTTTCCACAGCAAGTT 240
QY 241 TTACTTGGGATCTCTGAGCCTTAGCAATAGTGTGAGGTTGACTTCTGGAGCCATCCCG 300
Db 241 TTACTTGGGATCTCTGAGCCTTAGCAATAGTGTGAGGTTGACTTCTGGAGCCATCCCG 300
QY 301 TTTCCCGCCCGCCAAAAGAGCGAGATTTAAGCGGACGCTGGGCCAGAGCTGGGAA 360
Db 301 TTTCCCGCCCGCCAAAAGAGCGAGATTTAAGCGGACGCTGGGCCAGAGCTGGGAA 360
QY 361 ATGGCCCGCGAGCGAGCTCTCTCTCTGATGCTTTTGCAGACCGCGGTCTG 420
Db 361 ATGGCCCGCGAGCGAGCTCTCTCTCTGATGCTTTTGCAGACCGCGGTCTG 420
QY 421 CAGGGCGCTTGCCTGCTGAGTCGAGGGCTGCGGGGAACTAGGGCGCGGGGGTG 480
Db 421 CAGGGCGCTTGCCTGCTGAGTCGAGGGCTGCGGGGAACTAGGGCGCGGGGGTG 480
QY 481 GAAAAATCGAACTAGCTTTTCTTGGCTTGGAGTTTGTCTAACTTTGGAGCACTGC 540
Db 481 GAAAAATCGAACTAGCTTTTCTTGGCTTGGAGTTTGTCTAACTTTGGAGCACTGC 540
QY 541 TCAACCCCTATCCGAAGCCCTCTCCCTACTTTCTGGCTCCAGACCCCGTGAGGAGTGC 600
Db 541 TCAACCCCTATCCGAAGCCCTCTCCCTACTTTCTGGCTCCAGACCCCGTGAGGAGTGC 600
QY 601 CTACCCTGAACTGCAGATAGGGTCCCTCGCCCCAGGACGTGCCCTCCCGCGGTGT 660
Db 601 CTACCCTGAACTGCAGATAGGGTCCCTCGCCCCAGGACGTGCCCTCCCGCGGTGT 660
QY 661 CCCGCTCTCGGGAGTGACTTTTGGAACCGCCACTCCCTTCCCCCACTAGATGCTTT 720
Db 661 CCCGCTCTCGGGAGTGACTTTTGGAACCGCCACTCCCTTCCCCCACTAGATGCTTT 720
QY 721 TAAATAAATCTGAGTCTCACTTGAAGCTGAGCTAAGGCTGGGGCTCCCTTGAACCTGG 780
Db 721 TAAATAAATCTGAGTCTCACTTGAAGCTGAGCTAAGGCTGGGGCTCCCTTGAACCTGG 780
QY 781 AACTCGGGTTTATTTCCAAATGTCAGCTGTCAGTTTTCCTCCAGTCAATCTCCAAACAGG 840
Db 781 AACTCGGGTTTATTTCCAAATGTCAGCTGTCAGTTTTCCTCCAGTCAATCTCCAAACAGG 840
QY 841 AAGTTCTTCCCTGAGTGTGCGGAGAGGCTGAGCAAAACCCACAGCAGATCCGACCG 900
Db 841 AAGTTCTTCCCTGAGTGTGCGGAGAGGCTGAGCAAAACCCACAGCAGATCCGACCG 900
QY 901 GGTTCACCTCAGAACGAATGCTTGGCGGTGGGGCGCGAAGAGTGGCTTGGGA 960
Db 901 GGTTCACCTCAGAACGAATGCTTGGCGGTGGGGCGCGAAGAGTGGCTTGGGA 960
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Db 961 TCTCAATCTTCAACCATTTTCCACCATTTTGGTGAGACCTGGGGTGAGGTCCTTAGGT 1020
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Db 1021 GGGAGGCTCCTGAGAGAGGCTACCTCGGGCTTCCCACTCTGGCAATGTTCTTTT 1080
QY 1081 GCCTGGAAAATTAAGTATGTTAGTTTGAACGTTTGAACGAACTTCTCTTTTCG 1140
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Db 1141 CTAGGCTTTATGATTTGCAATGCTGTGTAATTAAGAGGCTCTCTCAAAAGTACTGA 1200

QY 1201 TAATGAACATGTAAAGCAATCACTCACTTCTAAAGTTACATTCATCTGATCTTAATTGA 1260
Db 1201 TAATGAACATGTAAAGCAATCACTCACTTCTAAAGTTACATTCATCTGATCTTAATTGA 1260
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Db 1261 TTTTCACTAGGCATAGGAGGTAGGAGCTAAATAAGCTTTATTTTACTAGAAGTTAACT 1320
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Db 1321 GGAATTCAGATTATATAACTCTTTTTCAGGTTTACAAAGAACATAAATACTGGTTCTCG 1380
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAACTTATAGTTGACAGTGAATTTGCCCTGTAG 1440
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Db 1621 TATGATCTTAAACATCAGCTGCATTTAGAGTTGAATAATAAAATTCATGTGTGAGCAG 1680
QY 1681 AAATATTCATTTTACAAAGTGTAAATGAGTCCCAGCCATGTGTGCACTGTTCAAGCC 1740
Db 1681 AAATATTCATTTTACAAAGTGTAAATGAGTCCCAGCCATGTGTGCACTGTTCAAGCC 1740
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Db 1801 GATGACAATTAAGCAATGAGCAGAAGATATACACATCAGGAATCATGGTGTGTGTA 1860
QY 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGAGACATGAAGA 1920
Db 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGAGACATGAAGA 1920
QY 1921 AATAAGAATGATATTGACTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
Db 1921 AATAAGAATGATATTGACTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
QY 1981 TTTGGATTTAAAACGGGTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
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Db 2101 CCTCCCTACTACTAGTGTAGGAGCACTCCCCAGTCTTGACAACCAAAATGCTCTCT 2160
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QY 2221 AATAAACAGTAGTGTCTGGGAGTAGAGGCCAAGAGTAGGTAAATGGGCTCAGAGAGGA 2280
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QY 2341 ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGTGAAGAGCAGAATG 2400
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Db 2341 ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGTGAAGAGCAGAATG 2400
QY 2401 AAGGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAAAGCTGTTACACAGTCCAGGCAAG 2460
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QY 2461 AGGTAGTGGAGTGGCTGGTGGGAACAGAAAGAGGAGTGACAAACATTTGCTCCTGAA 2520
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QY 2521 TATATTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAATTTGG 2580
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QY 2641 GTTCAAGACCAGGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700
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QY 2881 TGACTTTGTTCTTTATTTTAAATTTATTGGCTGAGCAGTGGGGTAAATGGCAATGCCAT 2940
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QY 2941 TTCTGAGATGTTGAAGCAGAGGAAGAGCAGTTTGGGGTAAATCAAGAGATCTGCATTTG 3000
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QY 3001 GGACATGTTAAGTTTGAGATTCCAGTTCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT 3060
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Db 3121 TTGTGGCTGAGGCAAGGTAGATCATTTGAGTCAAGAGTTTGGACAAGCTTGGCCAAACA 3180
QY 3181 TGGTGAACCCCATGCTCTACTTAAATAACAAAAATTTAGCCCTGGTGTGGTGGCGCACGCCCT 3240
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Db 3181 TGGTGAACCCCATGCTCTACTTAAATAACAAAAATTTAGCCCTGGTGTGGTGGCGCACGCCCT 3240
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Db 3301 TTGCAAGTGAAGTGTGCACTGCACTCCAGCCCTGGGTGATAGAGTGAGACTCTGT 3360
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QY 3421 TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATGGCTAGACACACACTTTAAC 3480
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QY 3481 ATTTTCTAGAATCCACCAGCTTTTASTGGAGTCTGCTAATCATAGTATTTGGAAATAGAT 3540
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QY 3601 ACCCAGGACTGTCATATATGAAAGAAAGACAGGACTGCAACTCACCTTTCACAAAAATGAGGA 3660
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QY 3961 AGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTTATGGAANAATCAACACCAG 4020
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QY 4081 ATGCATCTTTGAAGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAAGAGGAAG 4140
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QY 4141 GAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGGTGAANAATAGGACCTATTCTT 4200
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Db 4561 AGGTTGCAGGCGACGGAAATCCCTGGTTGGAGTTTCAGAGSTGGCTGTGCCTC 4620

Qy 4621 TCCAAATTTCTGGRAGGACATTTCTCAATCTAGAGTCTTACCTTATAATTTAGATGTA 4680

Db 4621 TCCAAATTTCTGGRAGGACATTTCTCAATCTAGAGTCTTACCTTATAATTTAGATGTA 4680

Qy 4681 TGAGACAGCCAAAGTCAATGGTTTAAATTTCTTTCTCCATGTCATATGGCTCAAGGGAA 4740

Db 4681 TGAGACAGCCAAAGTCAATGGTTTAAATTTCTTTCTCCATGTCATATGGCTCAAGGGAA 4740

Qy 4741 GTGCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA 4800

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Db 4861 AGGCCGAGCGGGTGGTCACAAGGTTCAGAGTTCAGACAGCAGCTGACCAACATGSGTAA 4920

Qy 4921 ACCCGTCTCTAAAAAATFACAAAAATTAGCTGGTCACAGTCATCGCACCTGTAGTCCCA 4980

Db 4921 ACCCGTCTCTAAAAAATFACAAAAATTAGCTGGTCACAGTCATCGCACCTGTAGTCCCA 4980

Qy 4981 GCTAATTTGGAAGGCTGAGCGAGGAGCATCGCTTGAACCTGGGAGCGGAAGTTGCACATGA 5040

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Db 5101 AAAAAAATAAAGAGAAATTCAGAGATCTCAGTATCATATGAATACCAAGGACAAA 5160

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Db 5221 AGAATAGCAATAATCAGTGAAGCTACCTATCTTTACAAGTCCCGCTTCTTATAACAATGC 5280

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Db 5281 CTCCTAGTTGACCCAGGTGAAATGACCATCTGTATTTCAATCATTTTCAATGCACATAA 5340

Qy 5341 AGGCAATTTTATCTATCAGAAACAAAGACATGGGTAAACAGATATGATTTTACATGTG 5400

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Qy 5401 AGGAGAACAAAGCTGATCTGACTGCTCTCCAAAGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460

Db 5401 AGGAGAACAAAGCTGATCTGACTGCTCTCCAAAGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460

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Db 5521 AACCTATAGAGGAAGTCAAAAGTTCCAGTCTTCTGCGCAAGGGTAAACAGATCCCCCTCTC 5580

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Db 5581 CTCACTCCTTCTCTTCCCTCAAGTGCCTCTTTTGGTGAAGGTGACACATCATGTGACC 5640

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Qy 5821 CAGAGATATACGTTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTATCTGG 5880

Db 5821 CAGAGATATACGTTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTATCTGG 5880

Qy 5881 GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGTTGAGAGGAGTGCC 5940

Db 5881 GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGTTGAGAGGAGTGCC 5940

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Db 6001 GTGGCAATCAAGGCTTTAACTTGTCTTTTGTAGAGCCCTCACCGTCTGGCACCC 6060

Qy 6061 TAGTCATTTGGAGTCAGTGGAAATGCTGTTTTTGTCTCATCTTGTTCATTGGAATTT 6120

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Qy 6121 TGTTCATATATTAAGAAAGAGCAGGTTTCAAGTGAGTAGGAACAAGGGGAAGTCTCT 6180

Db 6121 TGTTCATATATTAAGAAAGAGCAGGTTTCAAGTGAGTAGGAACAAGGGGAAGTCTCT 6180

Qy 6181 TAGTACCTTGCCCCAGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG 6240

Db 6181 TAGTACCTTGCCCCAGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG 6240

Qy 6241 AAGCATTTTCTCATTTATTTCTTTGGGACACCAAGCAGCTCCCTGGGAGACAGAAAAT 6300

Db 6241 AAGCATTTTCTCATTTATTTCTTTGGGACACCAAGCAGCTCCCTGGGAGACAGAAAAT 6300

Qy 6301 AATGGTCTCTCCACAGATGAAAGTCTCTAATTAACAAAAACATCTTCAGAGCACCTACTAT 6360

Db 6301 AATGGTCTCTCCACAGATGAAAGTCTCTAATTAACAAAAACATCTTCAGAGCACCTACTAT 6360

Qy 6361 TTTGCAAGAGCTGTTTAAAGTGTAGTACAGGGGCTTTGAGGTTGAGAGTCACTGTGGCTAT 6420

Db 6361 TTTGCAAGAGCTGTTTAAAGTGTAGTACAGGGGCTTTGAGGTTGAGAGTCACTGTGGCTAT 6420

Qy 6421 TCTCAGAACCCCAATCTGTTAGGGAATGAAATTTGATAGCAAGTAAATGTAGTTAAAGAG 6480

Db 6421 TCTCAGAACCCCAATCTGTTAGGGAATGAAATTTGATAGCAAGTAAATGTAGTTAAAGAG 6480

Qy 6481 ACCCCATGAGGTCTTAAAGCAGGAGCAAAATGCTTTAGGTTGTCAAGGAAAAAATG 6540

Db 6481 ACCCCATGAGGTCTTAAAGCAGGAGCAAAATGCTTTAGGTTGTCAAGGAAAAAATG 6540

Qy 6541 ATCACAATTCAGCTGGGGATCAAGATAGCCCTCTGGAATCTTTGAGGAGAGTGGATTCCA 6600

Db 6541 ATCACAATTCAGCTGGGGATCAAGATAGCCCTCTGGAATCTTTGAGGAGAGTGGATTCCA 6600

Qy 6601 TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGCAGGAGCAACCATGCCAAGTAGGA 6660

Db 6601 TTAGGTGAGGTTGAAGATGATGGGAGGTCTACACAGCAGGAGCAACCATGCCAAGTAGGA 6660

Db	8821	TTACACACGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGATTTTC	8885
Qy	8881	CCTCAATGAAGTGAGTAAGCTCTCTCATTTTGAGATGGTATAATGAAGACCCAAAGTG	8940
Db	8881	CCTCAATGAAGTGAGTAAGCTCTCTCATTTTGAGATGGTATAATGAAGACCCAAAGTG	8940
Qy	8941	GCTTAGAGGATGCCAGGTCCTTCCATGAGGCCACTGGGGTTCGGGTGCACATTAATAAAA	9000
Db	8941	GCTTAGAGGATGCCAGGTCCTTCCATGAGGCCACTGGGGTTCGGGTGCACATTAATAAAA	9000
Qy	9001	AAAATCTAACCGAGCATTCAGGAATGCTAGATTTCTGGGAAATCAGTTACACATGTCA	9060
Db	9001	AAAATCTAACCGAGCATTCAGGAATGCTAGATTTCTGGGAAATCAGTTACACATGTCA	9060
Qy	9061	AAAGAGTCCTTTTTTTTTTTTTGAGACTCTATTGCCAGGCTGGAGTGCATATGCCATGAT	9120
Db	9061	AAAGAGTCCTTTTTTTTTTTTTGAGACTCTATTGCCAGGCTGGAGTGCATATGCCATGAT	9120
Qy	9121	CTGGCTCACGTAAACCTCTGGCTCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA	9180
Db	9121	CTGGCTCACGTAAACCTCTGGCTCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCA	9180
Qy	9181	AGTAGCTGGGATTACAGGCGTGACACACATGCCCGCTAATTTTGTATTTTAGTAGA	9240
Db	9181	AGTAGCTGGGATTACAGGCGTGACACACATGCCCGCTAATTTTGTATTTTAGTAGA	9240
Qy	9241	GACAGGGTTTACACATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACTCGTGATCGCC	9300
Db	9241	GACAGGGTTTACACATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACTCGTGATCGCC	9300
Qy	9301	TGCTCGGCTCCCAAAGTCTGAGATTACAGTGTGAGCCACCCCTGCCAGCGGTCAA	9360
Db	9301	TGCTCGGCTCCCAAAGTCTGAGATTACAGTGTGAGCCACCCCTGCCAGCGGTCAA	9360
Qy	9361	AGAGTCTTAAT	9420
Db	9361	AGAGTCTTAAT	9420
Qy	9421	GCTGCATAAATGTGGTACAAAGTCTCTCTTTGAAGGCGAGTGCCTTCAGGATACCATAT	9480
Db	9421	GCTGCATAAATGTGGTACAAAGTCTCTCTTTGAAGGCGAGTGCCTTCAGGATACCATAT	9480
Qy	9481	ACAGCTCAGAAGTTCTCTTTTAGGCATTAATTTTAGCAAGATATCTCATCTCTCTT	9540
Db	9481	ACAGCTCAGAAGTTCTCTTTTAGGCATTAATTTTAGCAAGATATCTCATCTCTCTT	9540
Qy	9541	TTAAACCATTTCTTTTGTGGTTAGAAAAGTTATGTAGAAAAGTAAATGTGATTT	9600
Db	9541	TTAAACCATTTCTTTTGTGGTTAGAAAAGTTATGTAGAAAAGTAAATGTGATTT	9600
Qy	9601	ACGCTCATTTGAGAAAAGCTATAAATGAATACAATTAAGAGTCTTATTTAAATAGCCAG	9660
Db	9601	ACGCTCATTTGAGAAAAGCTATAAATGAATACAATTAAGAGTCTTATTTAAATAGCCAG	9660
Qy	9661	TGAAAACATTTAACAACTGTCTATTACCTGTTAGTATTTAGTGTGCAATTAATAATGCA	9720
Db	9661	TGAAAACATTTAACAACTGTCTATTACCTGTTAGTATTTAGTGTGCAATTAATAATGCA	9720
Qy	9721	TATACCTTAATAAATGTATATTTGATATGATATACGTGATATTTATTTAGAGTCTTGTT	9780
Db	9721	TATACCTTAATAAATGTATATTTGATATGATATACGTGATATTTATTTAGAGTCTTGTT	9780
Qy	9781	ATCTGTGTATATACTTAATCGTTTGTCAATTTTGGAGACATTTATTTGCTTCAATTT	9840
Db	9781	ATCTGTGTATATACTTAATCGTTTGTCAATTTTGGAGACATTTATTTGCTTCAATTT	9840
Qy	9841	CHTTACATTTTCTCTTAGGAAATATTTTCAATCAACTGTGTAGCCGAATTAATCGTGT	9900
Db	9841	CHTTACATTTTCTCTTAGGAAATATTTTCAATCAACTGTGTAGCCGAATTAATCGTGT	9900
Qy	9901	TCCTTACTCTAGGACATTCGCTTAAGTGTGAAGACATTTGGTATTTTACAGCAAAAC	9960
Db	9901	TCCTTACTCTAGGACATTCGCTTAAGTGTGAAGACATTTGGTATTTTACAGCAAAAC	9960

RESULT 11
US-09-503-444A-5
; Sequence 5, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta

QY 961 TCTGAATTTCTTACCATTCCACCACCTTTTGGTGAGACCTGGGGTGAGGTTCTTAGGGT 1020
Db 961 TCTGAATTTCTTACCATTCCACCACCTTTTGGTGAGACCTGGGGTGAGGTTCTTAGGGT 1020
QY 1021 GGGAGGCTCCTGAGAGAGGCTTACCCTGGGCTTTCCCCACTCTTGGCAATTTGTTCTTTT 1080
Db 1021 GGGAGGCTCCTGAGAGAGGCTTACCCTGGGCTTTCCCCACTCTTGGCAATTTGTTCTTTT 1080
QY 1081 GCGTGAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAAATCTCTTTTCGG 1140
Db 1081 GCGTGAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAAATCTCTTTTCGG 1140
QY 1141 CTAGGCTTTATTTGATTTGCAATGTGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200
Db 1141 CTAGGCTTTATTTGATTTGCAATGTGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200
QY 1201 TAATGAACATGTAAAGCAATGCACCTCTTAAGTTACATTCATATCTGATCTTATTTGA 1260
Db 1201 TAATGAACATGTAAAGCAATGCACCTCTTAAGTTACATTCATATCTGATCTTATTTGA 1260
QY 1261 TTTTCTACTAGGATAGGAGGTAGAGCTAATATACGTTTATTTTACTAGAACTTAAC 1320
Db 1261 TTTTCTACTAGGATAGGAGGTAGAGCTAATATACGTTTATTTTACTAGAACTTAAC 1320
QY 1321 GGAATTCAGATATATAACTCTTTTCAGGTTACAAAGAACATAAATATCTGGTTTCTG 1380
Db 1321 GGAATTCAGATATATAACTCTTTTCAGGTTACAAAGAACATAAATATCTGGTTTCTG 1380
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTAGAGTATTTGCCCTGTAG 1440
Db 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTAGAGTATTTGCCCTGTAG 1440
QY 1441 TGTAGCACAGTGTCTGTGGGTCACACGCGGCTTCAGCACAGACCTTTGAGTTTGGTA 1500
Db 1441 TGTAGCACAGTGTCTGTGGGTCACACGCGGCTTCAGCACAGACCTTTGAGTTTGGTA 1500
QY 1501 CTAGTGTATCCACATTTTACACATGACAAAGATGAGGCTAGGCGCTGCTTCCTGG 1560
Db 1501 CTAGTGTATCCACATTTTACACATGACAAAGATGAGGCTAGGCGCTGCTTCCTGG 1560
QY 1561 CAAATTTATTCATGTATACACTGGGCTTTGGTGCGAGAGCTCATGCTPCCACTTCATAGC 1620
Db 1561 CAAATTTATTCATGTATACACTGGGCTTTGGTGCGAGAGCTCATGCTPCCACTTCATAGC 1620
QY 1621 TATGATTTTAAACATCAACACTGCATTTAGAGTTGAATTAATAAATTTTCAATTTGAGCAG 1680
Db 1621 TATGATTTTAAACATCAACACTGCATTTAGAGTTGAATTAATAAATTTTCAATTTGAGCAG 1680
QY 1681 AAATATTTCAATTTTAAAGTGTAAATGATCCAGCCATGTTTGCACTGTTCAAGCCC 1740
Db 1681 AAATATTCATTTTAAAGTGTAAATGATCCAGCCATGTTTGCACTGTTCAAGCCC 1740
QY 1741 CAAGGAGAGAGGAGGAAACAGCTTTTACCCTTTGATATTTTGGCATTTAGTGGGAGA 1800
Db 1741 CAAGGAGAGAGGAGGAAACAGCTTTTACCCTTTGATATTTTGGCATTTAGTGGGAGA 1800
QY 1801 GATGACAAATGAAGCAATGAGCAAGAGATATACACATCAGGAATCATGGGTGTGTGA 1860
Db 1801 GATGACAAATGAAGCAATGAGCAAGAGATATACACATCAGGAATCATGGGTGTGTGA 1860
QY 1861 GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA 1920
Db 1861 GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGA 1920
QY 1921 AATAAGATGATATTCATCTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
Db 1921 AATAAGATGATATTCATCTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
QY 1981 TTGGATTTAAAGCGGTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
Db 1981 TTGGATTTAAAGCGGTTTCTCAGCACTACTCATGTGTGTGTGTGTGGGGGGGGGG 2040
QY 2041 CGGCGTGGGGTGGGAAGGGGACHTACCATCTGCATGTAGGATGCTAGCAGTATCTCTGT 2100

Db 2041 CGGCGTGGGGTGGGAAGGGGACTTACCATCTGCATGTAGGATGCTAGCAGTATCTCTGT 2100
QY 2101 CTTCCCTACTACTAGTGTCTAGGAGCACTCCCCAGTCTTGACAACCAAAATGTCTCT 2160
Db 2101 CTTCCCTACTACTAGTGTCTAGGAGCACTCCCCAGTCTTGACAACCAAAATGTCTCT 2160
QY 2161 AAATTTTGGCCACATGCTACCTTAGTAGCAAACTCCTGTTAAGAGCTCGGGTTGAAAA 2220
Db 2161 AAATTTTGGCCACATGCTACCTTAGTAGCAAACTCCTGTTAAGAGCTCGGGTTGAAAA 2220
QY 2221 AATAACAAGTAGTCTGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAAGGA 2280
Db 2221 AATAACAAGTAGTCTGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAAGGA 2280
QY 2281 GCCCAAAACAAGTTGTGCAGCGCCTGTAGGCTGTGTGTGAATTTAGCCAAGGAGTA 2340
Db 2281 GCCCAAAACAAGTTGTGCAGCGCCTGTAGGCTGTGTGTGAATTTAGCCAAGGAGTA 2340
QY 2341 ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTTGGCTGCTATGTGGAAGCAGAAAG 2400
Db 2341 ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTTGGCTGCTATGTGGAAGCAGAAAG 2400
QY 2401 AAGGAGCAACAGTAAAGAGCGGAGCCAGGAGGCTGTTTACACAGTCCAGGCAAG 2460
Db 2401 AAGGAGCAACAGTAAAGAGCGGAGCCAGGAGGCTGTTTACACAGTCCAGGCAAG 2460
QY 2461 AGGTAGTGGAGTGGGCTGGTGGGAACAGAAAGGAGTGACAAACCATTTGTCTCTGAA 2520
Db 2461 AGGTAGTGGAGTGGGCTGGTGGGAACAGAAAGGAGTGACAAACCATTTGTCTCTGAA 2520
QY 2521 TATATTTCTGAAGAAATTTGCTGAAGGATTTCTATGTTGTGAGAGAAAGAGAAATGG 2580
Db 2521 TATATTTCTGAAGAAATTTGCTGAAGGATTTCTATGTTGTGAGAGAAAGAGAAATGG 2580
QY 2581 CTGGGTGTAGTAGTCTGCCAAGGAGGCGCCAGGAGAGCAGATTTCTTGAGCTCAGGA 2640
Db 2581 CTGGGTGTAGTAGTCTGCCAAGGAGGCGCCAGGAGAGCAGATTTCTTGAGCTCAGGA 2640
QY 2641 GTTCAAGACACGCTGGGCAACACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
Db 2641 GTTCAAGACACGCTGGGCAACACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
QY 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCTTAGTCTCGGGAGGCTGAGGTGAGGGTA 2760
Db 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCTTAGTCTCGGGAGGCTGAGGTGAGGGTA 2760
QY 2761 TTTGCTTGAGCCAGGAAGTTGAGGCTGCAGTGAGCCTGCTGCTACTTCTCAGC 2820
Db 2761 TTTGCTTGAGCCAGGAAGTTGAGGCTGCAGTGAGCCTGCTGCTACTTCTCAGC 2820
QY 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTTGACCCCTGAAAAAGAGAGAGTTAAAGT 2880
Db 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTTGACCCCTGAAAAAGAGAGAGTTAAAGT 2880
QY 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAAATTTGCAATGCCAT 2940
Db 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAAATTTGCAATGCCAT 2940
QY 2941 TTCTGAGATGTTGAGGCAAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000
Db 2941 TTCTGAGATGTTGAGGCAAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000
QY 3001 GGACATGTTAAGTTTGAATTTCCAGTCCAGGCTTCCAGTGTGAGGCCACATAGGCAGTT 3060
Db 3001 GGACATGTTAAGTTTGAATTTCCAGTCCAGGCTTCCAGTGTGAGGCCACATAGGCAGTT 3060
QY 3061 CAGTGTAAAGATTTCAAGGCAAGGCTGGGCGAGGTTGCTCTCTCTGTTAATCCAGCACT 3120
Db 3061 CAGTGTAAAGATTTCAAGGCAAGGCTGGGCGAGGTTGCTCTCTCTGTTAATCCAGCACT 3120
QY 3121 TTGGTGGCTGAGGCAAGGTAGATCAATTTGAGGTCAGGACTTTGAGCAAGCTTTGCCAACA 3180

[illegible]

Qy	4261	GGCTGTGAAATGCAAGAAGACAAACAGTACCGGAGGCTACTGGAAGTACGGGTATGATGGG	4320
Db	4261	GGCTGTGAAATGCAAGAAGACAAACAGTACCGGAGGCTACTGGAAGTACGGGTATGATGGG	4320
Qy	4321	CAGGACCACTTCGAATTCCTGCCCTGCACACACTGGAATGAGAGCAGCAAGAACCCAGGGCC	4380
Db	4321	CAGGACCACTTCGAATTCCTGCCCTGCACACACTGGAATGAGAGCAGCAAGAACCCAGGGCC	4380
Qy	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCACAAGATTGCGGGCCAGCGAGAACAGGGCCCTAC	4440
Db	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCACAAGATTGCGGGCCAGCGAGAACAGGGCCCTAC	4440
Qy	4441	CTGGAGAGGCACTGCCCTGCACAGCTGCGACAGTTCCTGGAGCTGCGGAGCTGGGAGAGGTGTTTGG	4500
Db	4441	CTGGAGAGGCACTGCCCTGCACAGCTGCGACAGTTCCTGGAGCTGGGAGAGGTGTTTGG	4500
Qy	4501	GACCAACAAGGTATGGTGGAAACACACTTCTCTGCCCTTACTCTAGTGGCGAGAGTGGAGG	4560
Db	4501	GACCAACAAGGTATGGTGGAAACACACTTCTCTGCCCTTACTCTAGTGGCGAGAGTGGAGG	4560
Qy	4561	AGGTTGCAGGGCACGGAATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Db	4561	AGGTTGCAGGGCACGGAATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Qy	- 4621	TCCAAATTCGCGAAGGGACTTCTCTCAATCCTAGAGTCTCTACCTTATATTTAGATGTGA	4680
Db	4621	TCCAAATTCGCGAAGGGACTTCTCTCAATCCTAGAGTCTCTACCTTATATTTAGATGTGA	4680
Qy	4681	TGACACAGCCACCAAGTCATGGGTTTAATTTCTTTTCTCCATGCAATGGCTCAAAAGGAA	4740
Db	4681	TGACACAGCCACCAAGTCATGGGTTTAATTTCTTTTCTCCATGCAATGGCTCAAAAGGAA	4740
Qy	4741	GTGTCTATGCGCCCTTGCCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA	4800
Db	4741	GTGTCTATGCGCCCTTGCCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA	4800
Qy	4801	AAATTTCAGAAATCTCAAGCGCGGGCACGGTGGCTCACCCCTGTAATCCAGCACTTTGGG	4860
Db	4801	AAATTTCAGAAATCTCAAGCGCGGGCACGGTGGCTCACCCCTGTAATCCAGCACTTTGGG	4860
Qy	4861	AGCGCGAGGCGGTGCTCACAGGTCAGAGTTTCAGACCAAGCCCTGACCAACATGGTGAA	4920
Db	4861	AGCGCGAGGCGGTGCTCACAGGTCAGAGTTTCAGACCAAGCCCTGACCAACATGGTGAA	4920
Qy	4921	ACCGCTCTCTAAAAAATACAAAAATAGCTGGTCACAGTCAATGGCGCACTGTAGTCCCA	4980
Db	4921	ACCGCTCTCTCTAAAAAATACAAAAATAGCTGGTCACAGTCAATGGCGCACTGTAGTCCCA	4980
Qy	4981	GCTAATTTGGAAGCTGAGCGAGGACATCGCTTGAACCTGGGAGCGGAAGTTCGACTGA	5040
Db	4981	GCTAATTTGGAAGCTGAGCGAGGACATCGCTTGAACCTGGGAGCGGAAGTTCGACTGA	5040
Qy	5041	GCCAAGATCGCGCCACTGCACTCCAGCTTAGCGACGAGTGAGACTCCATCTTTAAAAAA	5100
Db	5041	GCCAAGATCGCGCCACTGCACTCCAGCTTAGCGACGAGTGAGACTCCATCTTTAAAAAA	5100
Qy	5101	AAAAAATAAAAAAAGAAATTCAGAGATCTCAGCTATCATATGAATACCAAGACAAA	5160
Db	5101	AAAAAATAAAAAAAGAAATTCAGAGATCTCAGCTATCATATGAATACCAAGACAAA	5160
Qy	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCTTTAGGTTAAAGTTCTTTTCAT	5220
Db	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCTTTAGGTTAAAGTTCTTTTCAT	5220
Qy	5221	AGAACATAGCAATAATCACTGGAAGCTTACCTATCTTACAAGTCCGCTTCTTATAACAATGC	5280
Db	5221	AGAACATAGCAATAATCACTGGAAGCTTACCTATCTTACAAGTCCGCTTCTTATAACAATGC	5280
Qy	5281	CTCCTAGGTTGACCCAGGTGAACACTGACCATCTGTATTCATCATTTTCAATGCAATAA	5340
Db	5281	CTCCTAGGTTGACCCAGGTGAACACTGACCATCTGTATTCATCATTTTCAATGCAATAA	5340

Qy	5341	AGGCCAATTTTATCTATCAACAACAAGACATGGGTAAACAGATATGTATTTACATGTG	5400
Db	5341	AGGGCAATTTTATCTATCAACAACAAGACATGGGTAAACAGATATGTATTTACATGTG	5400
Qy	5401	AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGAACACTGTGTAGCTTCCAATCTTAGG	5460
Db	5401	AGGAGAACAAGCTGATCTGACTGCTCTCCAAGTGAACACTGTGTAGCTTCCAATCTTAGG	5460
Qy	5461	ACACAAATGGTGCTCTCTCTGTAGCTTGTTTTTTTCTGAAAAGGTTATTTCTTCCTCC	5520
Db	5461	ACACAAATGGTGCTCTCTCTGTAGCTTGTTTTTTTCTGAAAAGGTTATTTCTTCCTCC	5520
Qy	5521	AACCTATAGAAGGAAGTGAAGTTCCAGTCTCTCTGGCAAGGTTAAACAGATCCCTCTC	5580
Db	5521	AACCTATAGAAGGAAGTGAAGTTCCAGTCTCTCTGGCAAGGTTAAACAGATCCCTCTC	5580
Qy	5581	CTCATCTTCTCTCTCTCTCAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACC	5640
Db	5581	CTCATCTTCTCTCTCTCTCAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACC	5640
Qy	5641	TCCTTCAGTGACCCTCTAGGGTCTGGGGCTTTGAACCTACTACCCCAAGACATCACCATG	5700
Db	5641	TCCTTCAGTGACCCTCTAGGGTCTGGGGCTTTGAACCTACTACCCCAAGACATCACCATG	5700
Qy	5701	AAAGTGGCTGAAGGATAAGCAGCAATGATGCCAAGGAGTTTCGAACCTTAAAGAGCTATTG	5760
Db	5701	AAAGTGGCTGAAGGATAAGCAGCAATGATGCCAAGGAGTTTCGAACCTTAAAGAGCTATTG	5760
Qy	5761	CCCAATGGGATGGGACCTACCAAGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAG	5820
Db	5761	CCCAATGGGATGGGACCTACCAAGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAG	5820
Qy	5821	CAGAGATATACGTNCCAGGTGGAGCACCAAGCCCTGGATCAGCCCTCATTTGTGATCTGG	5880
Db	5821	CAGAGATATACGTGCCAGGTGGAGCACCAAGCCCTGGATCAGCCCTCATTTGTGATCTGG	5880
Qy	5881	GGTATGTGACTGATGAGACCCAGGAGCTGAGAAAAATCTATTGGGGGTTGAGAGGAGTGCC	5940
Db	5881	GGTATGTGACTGATGAGACCCAGGAGCTGAGAAAAATCTATTGGGGGTTGAGAGGAGTGCC	5940
Qy	5941	TGAGGAGGTAAATTTATGGCAGTCAGATGAGGATCTCTCTTTGTAGGGGTGGGCTGAGG	6000
Db	5941	TGAGGAGGTAAATTTATGGCAGTCAGATGAGGATCTCTCTTTGTAGGGGTGGGCTGAGG	6000
Qy	6001	GTGGCAATCAAGGCTTTAACTTGTCTTTTCTGTGTTTAGAGCCCTCACCTCTGGCACCC	6060
Db	6001	GTGGCAATCAAGGCTTTAACTTGTCTTTTCTGTGTTTAGAGCCCTCACCTCTGGCACCC	6060
Qy	6061	TAGTCATTTGGAGTCATCAGTGGAAATGCTGTTTTGTGCTCATCTCTCTATTGGGAATTT	6120
Db	6061	TAGTCATTTGGAGTCATCAGTGGAAATGCTGTTTTGTGCTCATCTCTCTATTGGGAATTT	6120
Qy	6121	TGTTTCATAATATTAGGAAGAGCGAGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT	6180
Db	6121	TGTTTCATAATATTAGGAAGAGCGAGGTTCAAGTGAGTAGGAACAAGGGGGAAGTCTCT	6180
Qy	6181	TAGTACTCTGCCCGAGGACAGTGGCAAGAGGGCAGAGGGATCTGCAATCCATGGG	6240
Db	6181	TAGTACTCTGCCCGAGGACAGTGGCAAGAGGGCAGAGGGATCTGCAATCCATGGG	6240
Qy	6241	AAGCATTTTCTCATTTATATTCTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAAT	6300
Db	6241	AAGCATTTTCTCATTTATATTCTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAAT	6300
Qy	6301	AATGGGTTCTCCCAAGATGAAGTCTCTAAATCAACAAACATCTTCAGAGCACCTACTAT	6360
Db	6301	AATGGGTTCTCCCAAGATGAAGTCTCTAAATCAACAAACATCTTCAGAGCACCTACTAT	6360
Qy	6361	TTTTCGAAGAGCTGTTTAAAGGTAGTACAGGGCTTTGAGGTTGAGAAGTCACTCTGCTAT	6420
Db	6361	TTTTCGAAGAGCTGTTTAAAGGTAGTACAGGGCTTTGAGGTTGAGAAGTCACTCTGCTAT	6420
Qy	6421	TCTCAGAACCCAAATCTGTTAGGGAATGAAATTCATAGCAAGTAAATGTAGTTTAAAGAG	6480

D _b	6421	TCTCAGAAACCAAAATCTGTTAGGGGAATAAATTGATACCAAGTAAATGTACTTAAGAAG	6480
Q _y	6481	ACCCCATGAGTGTCCTAAACGACGCAGCAAGCAAATGCTTAGGTGTCAAGAAAGAATG	6540
D _b	6481	ACCCCATGAGTGTCCTAAACGACGCAGCAAGCAAATGCTTAGGTGTCAAGAAAGAATG	6540
Q _y	6541	ATCACATTCAGCTGGGGATCAAGATAGCGCTTCTGGATCTTCAAGGAGAAAGCTGATTCCA	6600
D _b	6541	AUCACATTCAGCTGGGGATCAAGATAGCGCTTCTGGATCTTCAAGGAGAAAGCTGATTCCA	6600
Q _y	6601	TTAGGTGAGTTGAGATGATGGGAGGTCTACACAGACGGAGACAACCATGCCAAGTAGGA	6660
D _b	6601	TTAGGTGAGTTGAGATGATGGGAGGTCTACACAGACGGAGACAACCATGCCAAGTAGGA	6660
Q _y	6661	GAGTATAAGGCATCTGGGAGATTAGAATAATTACTCTACTTAAACCTCAGTTTTGGGT	6720
D _b	6661	GAGTATAAGGCATCTGGGAGATTAGAATAATTACTCTACTTAAACCTCAGTTTTGGGT	6720
Q _y	6721	ASCTATCACTCACCAATTAATGCAATTTACCCCCTGAACATCTCTGGTGTAGGAAAAAGA	6780
D _b	6721	ASCTATCACTCACCAATTAATGCAATTTACCCCCTGAACATCTCTGGTGTAGGAAAAAGA	6780
Q _y	6781	GAATCAGAAAGAACGACGTCAATCAGAGTCCAAAGSGTCTTTTGGGATATGGGTTATGA	6840
D _b	6781	GAATCAGAAAGAACGACGTCAATCAGAGTCCAAAGSGTCTTTTGGGATATGGGTTATGA	6840
Q _y	6841	TCACTGGGTGTCAATTGAAGGATCCTAAGAAGGAGGACCAACGATCTCCCCCTTATATGGT	6900
D _b	6841	TCACTGGGTGTCAATTGAAGGATCCTAAGAAGGAGGACCAACGATCTCCCCCTTATATGGT	6900
Q _y	6901	AATGTGTTCTTAAGAAAGTTAGATGAGAGGTGAGAGACCCAGTTAGAAGCAATAAGCAT	6960
D _b	6901	AATGTGTTCTTAAGAAAGTTAGATGAGAGGTGAGAGACCCAGTTAGAAGCAATAAGCAT	6960
Q _y	6961	TTCCAGATGAGAGATAATGGTTCTTTGAATCCAAATAGTGCCACGTCTAAATTCAGATGG	7020
D _b	6961	TTCCAGATGAGAGATAATGGTTCTTTGAATCCAAATAGTGCCACGTCTAAATTCAGATGG	7020
Q _y	7021	GTGAATGAGAAAAATAAGAGAGAGAGAGAGGCAAGATGGTGCCCTAGTTTGTGATGCCCT	7080
D _b	7021	GTGAATGAGAAAAATAAGAGAGAGAGAGAGGCAAGATGGTGCCCTAGTTTGTGATGCCCT	7080
Q _y	7081	CCTTCCCTGGGTCTCTTGTTCTCCACAGGAGGACCATGGGGCACFACGCTCTTAGCTGAACG	7140
D _b	7081	CCTTCCCTGGGTCTCTTGTTCTCCACAGGAGGACCATGGGGCACFACGCTCTTAGCTGAACG	7140
Q _y	7141	TGAGTGACACGAGCGCTGCAGACTACTGTGGGAGGAGACAAAACCTAGAGACTCAAGA	7200
D _b	7141	TGAGTGACACGAGCGCTGCAGACTACTGTGGGAGGAGACAAAACCTAGAGACTCAAGA	7200
Q _y	7201	GGGAGTGCATTTATGAGCTCTTTCATGTTTCAGGAGAGAGTTGAACCTPAAACATAGAAAT	7260
D _b	7201	GGGAGTGCATTTATGAGCTCTTTCATGTTTCAGGAGAGAGTTGAACCTPAAACATAGAAAT	7260
Q _y	7261	GCCTGACGAATCCTTGATNTTTCCTGTTCTGTTTCCCTCAAAAAGATTTCCCCCAT	7320
D _b	7261	GCCTGACGAATCCTTGATNTTTCCTGTTCTGTTTCCCTCAAAAAGATTTCCCCCAT	7320
Q _y	7321	TTAGGTTTCTCAGTTTCCTGATGCGGTGATCCCTAGCTGTGACCTCTCCCTGGAACTG	7380
D _b	7321	TTAGGTTTCTCAGTTTCCTGATGCGGTGATCCCTAGCTGTGACCTCTCCCTGGAACTG	7380
Q _y	7381	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTTCATTTCCCTCCGTCACCTCAGAG	7440
D _b	7381	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTTCATTTCCCTCCGTCACCTCAGAG	7440
Q _y	7441	ACATACACCTATGTCATTTTCATTTCCCTATTTTGGGAGAGGACTCCCTTAAATTTGGGGGA	7500
D _b	7441	ACATACACCTATGTCATTTTCATTTCCCTATTTTGGGAGAGGACTCCCTTAAATTTGGGGGA	7500
Q _y	7501	CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTTGAACCCCTGGGAGGTGGCTAGTCAT	7560

Db 7501 CTTACATGATTCAATTTAAACATCTGAGAAAAGCTTTGAACCCCTGGGAGCTGGCTAGTCAT 7560
Qy 7561 AACCTTACCAGATTTTACACATGATCTATGCATTTCTGACCCGTTCAACTTTTCT 7620
Db 7561 AACCTTACCAGATTTTACACATGATCTATGCATTTCTGACCCGTTCAACTTTTCT 7620
Qy 7621 TTGAATCCCTCTCTCTGTTTACCAGTAACCTCATCTGTCAACCAAGCCTTGGGATTCCT 7680
Db 7621 TTGAATCCCTCTCTCTGTTTACCAGTAACCTCATCTGTCAACCAAGCCTTGGGATTCCT 7680
Qy 7681 CATCTGATGTGATGAGTGTGCACAGCTATGAAGGCTGTACACTGCACGAATGAAGAG 7740
Db 7681 CATCTGATGTGATGAGTGTGCACAGCTATGAAGGCTGTACACTGCACGAATGAAGAG 7740
Qy 7741 GCACCTGTCCAGAAAAAGCATCGGCTATCTGTGGGTAGTATGATGGTGTTTTAGC 7800
Db 7741 GCACCTGTCCAGAAAAAGCATCGGCTATCTGTGGGTAGTATGATGGTGTTTTAGC 7800
Qy 7801 AGGTAGGAGCAATATCTTTGAAGGGTTGTGAAGAGGTGTTTTTCTTAATTGGCATGA 7860
Db 7801 AGGTAGGAGCAATATCTTTGAAGGGTTGTGAAGAGGTGTTTTTCTTAATTGGCATGA 7860
Qy 7861 AGGTGTACATACAGATTGCAAAAGTTTAAATGGTGCCCTTCAATTTGGGATGCTACTAGTAT 7920
Db 7861 AGGTGTACATACAGATTGCAAAAGTTTAAATGGTGCCCTTCAATTTGGGATGCTACTAGTAT 7920
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US-09-503-444A-7

Query Match 100.0%; Score 10823; DB 4; Length 10825;
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QY TAGTACCTCTGCCCCAGGGCACAGTCAGTGGGAAGAGGGGACAGAGGGATCTGGCATCCATGGG 6240
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RESULT 13
US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724, 394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
US-08-724-394A-20

Query Match 100.0%; Score 10823; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Qy 1621 TATGATTTTAAACATCACACTGCATTTAGAGTTGAATAATAAATTTTCATGTTGAGCAG 1680
 Db 193924 TATGATTTTAAACATCACACTGCATTTAGAGTTGAATAATAAATTTTCATGTTGAGCAG 193983
 Qy 1681 AAATATTCATTTTACAAAGTGAATGAGTCCAGGCCATGTTGACACTGTTCAAGCCC 1740
 Db 193984 AAATATTCATTTTACAAAGTGAATGAGTCCAGGCCATGTTGACACTGTTCAAGCCC 194043
 Qy 1741 CAAGGAGAGAGCAGGGAACAGTCTTTACCTTTTGCATTTTGTGAGTGGGAGA 1800
 Db 194044 CAAGGAGAGAGCAGGGAACAGTCTTTACCTTTTGCATTTTGTGAGTGGGAGA 194103
 Qy 1801 GATGACAATAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGTGTCTGA 1860
 Db 194104 GATGACAATAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGTGTCTGA 194163
 Qy 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTTGAGCAGACATGAAGGA 1920
 Db 194164 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTTGAGCAGACATGAAGGA 194223
 Qy 1921 AATAGATGATATTGACTGGGAGCAGTATTTCCAGGCAACCTGAGTGGGCTGGCAAG 1980
 Db 194224 AATAGATGATATTGACTGGGAGCAGTATTTCCAGGCAACCTGAGTGGGCTGGCAAG 194283
 Qy 1981 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
 Db 194284 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 194343

Qy 2041 CGGGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCTGT 2100
 Db 194344 CGGGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCTGT 194403
 Qy 2101 CCTCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTTGACAAACCAAAATGTCTCT 2160
 Db 194404 CCTCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTTGACAAACCAAAATGTCTCT 194463
 Qy 2161 AAACCTTCCCACTGTCACTACCTAGTAGACAAACCTCTGTGTTAAGAGCTCGGGTTGAAAA 2220
 Db 194464 AAACCTTCCCACTGTCACTACCTAGTAGACAAACCTCTGTGTTAAGAGCTCGGGTTGAAAA 194523
 Qy 2221 AATAAACAAAGTAGTCTGGGAGTAGAGCCAAAGTAGGTATGCGCTCAGAAGAGGA 2280
 Db 194524 AATAAACAAAGTAGTCTGGGAGTAGAGCCAAAGTAGGTATGCGCTCAGAAGAGGA 194583
 Qy 2281 GCCACAACAAAGTTGTCCAGGCGCTGTAGGCTGTGTGTGAATTTCTAGGCAAGAGGTA 2340
 Db 194584 GCCACAACAAAGTTGTCCAGGCGCTGTAGGCTGTGTGTGAATTTCTAGGCAAGAGGTA 194643
 Qy 2341 ACAGTGATCTGTCAAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAAGCAGAATG 2400
 Db 194644 ACAGTGATCTGTCAAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAAGCAGAATG 194703
 Qy 2401 AAGGAGCAACAGTAAAAAGCAGGAGCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG 2460
 Db 194704 AAGGAGCAACAGTAAAAAGCAGGAGCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG 194763
 Qy 2461 AGGTAGTGAGTGCGCTGGTGGGAACAGAAAGAGGAGTGCACAAACCATTTGCTCCTGAA 2520
 Db 194764 AGGTAGTGAGTGCGCTGGTGGGAACAGAAAGAGGAGTGCACAAACCATTTGCTCCTGAA 194823
 Qy 2521 TATATTTGAAGAAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAAATTTGG 2580
 Db 194824 TATATTTGAAGAAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAAATTTGG 194883
 Qy 2581 CTGGGTGTAGTACCTCATGCCAAGGAGGAGCCAAAGAGAGCAGATTCTCTGAGCTCAGGA 2640
 Db 194884 CTGGGTGTAGTACCTCATGCCAAGGAGGAGCCAAAGAGAGCAGATTCTCTGAGCTCAGGA 194943
 Qy 2641 GTTCAAGACCAAGCTGGGCAACACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
 Db 194944 GTTCAAGACCAAGCTGGGCAACACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 195003
 Qy 2701 GCTGGGTGTGGCATGACCATGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGTA 2760
 Db 195004 GCTGGGTGTGGCATGACCATGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGTA 195063
 Qy 2761 TTGCTTTGAGCCAGGAAGTTGAGGCTGCAGTGCAGCATGACTGTGCCACTGTACTTTCAGC 2820
 Db 195064 TTGCTTTGAGCCAGGAAGTTGAGGCTGCAGTGCAGCATGACTGTGCCACTGTACTTTCAGC 195123
 Qy 2821 CTAGGTGACAGAGCAAGACCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTAAAGT 2880
 Db 195124 CTAGGTGACAGAGCAAGACCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTAAAGT 195183
 Qy 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGCGCTGAGCAGTGGGTAATTTGGCAATGCCAT 2940
 Db 195184 TGACTTTGTTCTTTATTTTAAATTTTATTTGCGCTGAGCAGTGGGTAATTTGGCAATGCCAT 195243
 Qy 2941 TTCTGAGATGGTGAAGGCAAGAGGAAAGACAGTTTTGGGTAATCAAGGATCTGCATTTG 3000
 Db 195244 TTCTGAGATGGTGAAGGCAAGAGGAAAGACAGTTTGGGGTAATCAAGGATCTGCATTTG 195303
 Qy 3001 GGACATGTTAAAGTTTGAATTCAGTTCAGGCTTCCAAAGTGTGGGCCACATAGGCAGTT 3060
 Db 195304 GGACATGTTAAAGTTTGAATTCAGTTCAGGCTTCCAAAGTGTGGGCCACATAGGCAGTT 195363
 Qy 3061 CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCAAGGCTGCTCTCTGTAATCCAGCACT 3120
 Db 195364 CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCAAGGCTGCTCTCTGTAATCCAGCACT 195423

QY 3121 TTGGTGGCTGAGCGAGGTAGATCATTTGAGGTCAGAGTTTGAGACAAGCTTTGGCCAAACA 3180
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Db 195424 TTGGTGGCTGAGCGAGGTAGATCATTTGAGGTCAGAGTTTGAGACAAGCTTTGGCCAAACA 195483
QY 3181 TGGTGAACCCCATGCTCTACTTAAATAATACAAAAATTAGCCTGGTGGTGGCGCCACGCCCT 3240
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Db 195484 TGGTGAACCCCATGCTCTACTTAAATAATACAAAAATTAGCCTGGTGGTGGCGCCACGCCCT 195543
QY 3241 ATAGTCCCAAGTTTTCAGGAGGCTTAGGTAGGAGAACTCCCTTGAACCCAGGAGGTGCAGG 3300
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Db 195544 ATAGTCCCAAGTTTTCAGGAGGCTTAGGTAGGAGAACTCCCTTGAACCCAGGAGGTGCAGG 195603
QY 3301 TTGCAGTGAAGTATGTCGCACTGCCTCCAGCCTGGGTGATAGTGAAGTCTGT 3360
|||||
Db 195604 TTGCAGTGAAGTATGTCGCACTGCCTCCAGCCTGGGTGATAGTGAAGTCTGT 195663
QY 3361 CTCAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 3420
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Db 195664 CTCAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 195723
QY 3421 TCTAATTTGCCCTGAGCACCAACTCTCTGAGTTCAACTTACCATGGCTAGACACACCTTTAAC 3480
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Db 195724 TCTAATTTGCCCTGAGCACCAACTCTCTGAGTTCAACTTACCATGGCTAGACACACCTTTAAC 195783
QY 3481 ATTTTCTAGAATCCACCAAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 3540
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Db 195784 ATTTTCTAGAATCCACCAAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 195843
QY 3541 CTGGGGGAGTGGGGGTGGCGCCAGCTGTGGCAGAGAAAGACACAAAGAAAGAGC 3600
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Db 195844 CTGGGGGAGTGGGGGTGGCGCCAGCTGTGGCAGAGAAAGACACAAAGAAAGAGC 195903
QY 3601 ACCCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCTTTCACAAATGAGGA 3660
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Db 195904 ACCCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCTTTCACAAATGAGGA 195963
QY 3661 CCAGACACAGCTGATGATGAGTTGATGAGTGTGAGGCTGTGGAGCCTCAACATCTGCTCCC 3720
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Db 195964 CCAGACACAGCTGATGATGAGTTGATGAGGCTGTGGAGCCTCAACATCTGCTCCC 196023
QY 3721 CTCCTACTACATGTTTAAAGCCCTGTGCTCTGCTCCAGGTTTCACACTCTCTGCACTA 3780
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Db 196024 CTCCTACTACATGTTTAAAGCCCTGTGCTCTGCTCCAGGTTTCACACTCTCTGCACTA 196083
QY 3781 CCTCTTCAATGGTGCCTCAGACAGGAGCCTTGGTCTTTCCTTGTTCGAACTTTGGGCTA 3840
|||||
Db 196084 CCTCTTCAATGGTGCCTCAGACAGGAGCCTTGGTCTTTCCTTGTTCGAACTTTGGGCTA 196143
QY 3841 CGTGATGACCAAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCGGAAC 3900
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Db 196144 CGTGATGACCAAGCTGTTCGTGTTCTATGATNATGAGAGTCGCCGTGTGGAGCCCGGAAC 196203
QY 3901 TCCATGGGTTCCAGTAGAATTTCAAGCCAGATGTGGCTGAGTGCAGAGTCTGAA 3960
|||||
Db 196204 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGAGTGCAGAGTCTGAA 196263
QY 3961 AGGGTGGGATACATGTTTCACTGTGTGACTTCTGGACTATTATGAAATACAAACACAG 4020
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Db 196264 AGGGTGGGATACATGTTTCACTGTGTGACTTCTGGACTATTATGAAATACAAACACAG 196323
QY 4021 CAAGGGTATGTGGAGAGGGGCTCACCTTCTGAGTGTGCAGAGCTTTTCATCTTTTC 4080
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Db 196324 CAAGGGTATGTGGAGAGGGGCTCACCTTCTGAGTGTGCAGAGCTTTTCATCTTTTC 196383
QY 4081 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTTGTGGAGCAGGGAAGGGAAG 4140
|||||
Db 196384 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTTGTGGAGCAGGGAAGGGAAG 196443
QY 4141 GAATTTGCTTCTGAGATCATTTGGTCTCTGGGATGGTGAATAGGGACCTATTTCCTT 4200
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Db 196444 GAATTTGCTTCTGAGATCATTTGGTCTCTGGGATGGTGAATAGGGACCTATTTCCTT 196503
QY 4201 TGGTTCCAGTTTAAAGGCTGGGATTTTCCAGAGTCCACACCTTGCAGGTCATCTTG 4260
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Db 196504 TGGTTGCAGTTTAAACAGCTGGGATTTTCCAGAGTCCACACCTTCAGGTCATCTCG 196563
QY 4261 GGCTGTGAAATGCAAGAGACACAGTACCAGGGCTACTGGAGTACGGGTATGATGGG 4320
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Db 196564 GGCTGTGAAATGCAAGAGACACAGTACCAGGGCTACTGGAGTACGGGTATGATGGG 196623
QY 4321 CAGGACCACTTGAATTTCTGCCCTGACACACTGGAATGGAGACAGCAACCCAGGGCC 4380
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Db 196624 CAGGACCACTTGAATTTCTGCCCTGACACACTGGAATGGAGACAGCAACCCAGGGCC 196683
QY 4381 TGGCCCAACCAAGCTGGAGTGGGAAAGCCACAAGATTGGGCCAGGAGAGGCTTAC 4440
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Db 196684 TGGCCCAACCAAGCTGGAGTGGGAAAGCCACAAGATTGGGCCAGGAGAGGCTTAC 196743
QY 4441 CTGAGAGGGGACTGCCCTGCACAGCTGCAGCTGTGGAGCTGGGAGAGGTGTTTG 4500
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Db 196744 CTGAGAGGGACTGCCCTGCACAGCTGCAGCTGTGGAGCTGGGAGAGGTGTTTG 196803
QY 4501 GACCAACAAGTATGTTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAG 4560
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Db 196804 GACCAACAAGTATGTTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAG 196863
QY 4561 AGGTTGAGGCGACCGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGCTCTC 4620
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Db 196864 AGGTTGAGGCGACCGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGCTCTC 196923
QY 4621 TCCAAATTTCTGGGAAGGACTTCTCAATCCTAGAGTCTCTACCTTATTAATTTGAGATGA 4680
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Db 196924 TCCAAATTTCTGGGAAGGACTTCTCAATCCTAGAGTCTCTACCTTATTAATTTGAGATGA 196983
QY 4681 TGAGACAGCCACAAGTCTATGGGTTTAAATTTCTTCCATGCATATGGCTCAAGGGAA 4740
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Db 196984 TGAGACAGCCACAAGTCTATGGGTTTAAATTTCTTCCATGCATATGGCTCAAGGGAA 197043
QY 4741 GTGTCTATGGCCCTTGGCTTTTATTTAACCAATTAATCTTTTGTATATTTATACCTGTTAA 4800
|||||
Db 197044 GTGTCTATGGCCCTTGGCTTTTATTTAACCAATTAATCTTTTGTATATTTATACCTGTTAA 197103
QY 4801 AAATTCAGAAATGTCAAGGCGGGCAGCGTGGCTTCAACCTGTAATCCAGCAGCTTTGGG 4860
|||||
Db 197104 AAATTCAGAAATGTCAAGGCGGGCAGCGTGGCTTCAACCTGTAATCCAGCAGCTTTGGG 197163
QY 4861 AGGCGGAGGCGGGTGTCAACAAGTCAAGGTTTGAGCAGCCTGACCAACATGTTGAA 4920
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Db 197164 AGGCGGAGGCGGGTGTCAACAAGTCAAGGTTTGAGCAGCCTGACCAACATGTTGAA 197223
QY 4921 ACCGCTCTCTAAAAAATACAAAAATTTAGCTGGTTCAGAGTCATGCCACCTGTAGTCCCA 4980
|||||
Db 197224 ACCGCTCTCTAAAAAATACAAAAATTTAGCTGGTTCAGAGTCATGCCACCTGTAGTCCCA 197283
QY 4981 GCTAATTTGGAAGGCTGAGGCGAGGAGCATCGCTTGAACCTGGGAAGCGGAGTTGCACTGA 5040
|||||
Db 197284 GCTAATTTGGAAGGCTGAGGCGAGGAGCATCGCTTGAACCTGGGAAGCGGAGTTGCACTGA 197343
QY 5041 GCCAAGATCGCGCCACTGCACTCCAGCCTAGGACAGAGTGAAGTCTCTTAAAAAAA 5100
|||||
Db 197344 GCCAAGATCGCGCCACTGCACTCCAGCCTAGGACAGAGTGAAGTCTCTTAAAAAA 197403
QY 5101 AAAAAAATAAAAAAAGAGAAATTCAGAGTCTCAGGATCTCAGCTATCATATGATACCAAGACAA 5160
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Db 197404 AAAAAAATAAAAAAAGAGAAATTCAGAGTCTCAGGATCTCAGCTATCATATGATACCAAGACAA 197463
QY 5161 ATATCAAGTGAAGGCACTTATCAGAGTAGAAGAACTCTTTAGGTTAAAAAGTTCTTTTCAT 5220
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Db 197464 ATATCAAGTGAAGGCACTTATCAGAGTAGAAGAACTCTTTAGGTTAAAAAGTTCTTTTCAT 197523
QY 5221 AGACATAGCAATTAATCACTGAAGCTACCTATCTTACAAGTCCGCTCTTTATTAACAATGC 5280
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Db 197524 AGACATAGCAATTAATCACTGAAGCTACCTATCTTACAAGTCCGCTCTTTATTAACAATGC 197583
QY 5281 CTCCTAGGTTCCACCAGGTGAAGTGAAGTCACTCTGATTTCAATCATTTTCAATCCACATAA 5340
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[illegible]

QY	6421	TCTCAGAACCCAAATCTCGGTAGGGAATGAATTCATAGCAAGTAAATGTAGTTAAAGAAG	6480
Db	198724	TCTCAGAACCCAAATCTCGGTAGGGAATGAATTCATAGCAAGTAAATGTAGTTAAAGAAG	198783
QY	6481	ACCCATGAGGTCTTAAAGCAGGCAAGCAAAATGCTTAGGGTGTCAAAGAGAAAGAAATG	6540
Db	198784	ACCCATGAGGTCTTAAAGCAGGCAAGCAAAATGCTTAGGGTGTCAAAGAGAAAGAAATG	198843
QY	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAGCTGGATTCCA	6600
Db	198844	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAGCTGGATTCCA	198903
QY	6601	TTTAGTGTAGGTTGAAGATGATGGGAGGTCTACACAGACGAGCAACCATGCCCAAGTAGGA	6660
Db	198904	TTTAGTGTAGGTTGAAGATGATGGGAGGTCTACACAGACGAGCAACCATGCCCAAGTAGGA	198963
QY	6661	GAGTATAGGCATACTGGGAGATTAGAAATAATTACTTGTACCTTTAACCTGTAGTTGGCT	6720
Db	198964	GAGTATAGGCATACTGGGAGATTAGAAATAATTACTTGTACCTTTAACCTGTAGTTGGCT	199023
QY	6721	AGCTATCACTACCAAAATTTATGCATTTCTACCCCTGAACATCTGTGGTGTAGGGAAGAAG	6780
Db	199024	AGCTATCACTACCAAAATTTATGCATTTCTACCCCTGAACATCTGTGGTGTAGGGAAGAAG	199083
QY	6781	GAAATCAGAAAGAGCCAGCTCATACAGAGTCCAAGGCTTTTGGGANATTTGGGTTATGA	6840
Db	199084	GAAATCAGAAAGAGCCAGCTCATACAGAGTCCAAGGCTTTTGGGANATTTGGGTTATGA	199143
QY	6841	TCACATGGGGTGTCAATTGAAGGATCCTAAGAAGGAGGACCACCATCTCCCTTATATGGTG	6900
Db	199144	TCACATGGGGTGTCAATTGAAGGATCCTAAGAAGGAGGACCACCATCTCCCTTATATGGTG	199203
QY	6901	AAATGTGTGTTAAGAAATTTAGATGAGAGGTGAGAGACACAGTTAGAAAGCCAATAAGCAT	6960
Db	199204	AAATGTGTGTTAAGAAATTTAGATGAGAGGTGAGAGACACAGTTAGAAAGCCAATAAGCAT	199263
QY	6961	TTCCAGATGAGAGATAATGGTCTTTGAAATCCAAATAGTGCACAGGTCTAAATTTAGATGG	7020
Db	199264	TTCCAGATGAGAGATAATGGTCTTTGAAATCCAAATAGTGCACAGGTCTAAATTTAGATGG	199323
QY	7021	GTGAATGAGGAAATTAAGAGAGAGAGAGGCAAGATGTCCTAGGTTTGTGATGCCT	7080
Db	199324	GTGAATGAGGAAATTAAGAGAGAGAGAGGCAAGATGTCCTAGGTTTGTGATGCCT	199383
QY	7081	CTTCTCTGGGTCTTGTCTCCACAGGAGGAGCCATGGGCACTAGCTCTTAGCTGAAGG	7140
Db	199384	CTTCTCTGGGTCTTGTCTCCACAGGAGGAGCCATGGGCACTAGCTCTTAGCTGAAGG	199443
QY	7141	TCAGTGCACAGCCGCTCAGACCTACTGTGGGAGAGACAAACTAGAGACTCCAAGA	7200
Db	199444	TCAGTGCACAGCCGCTCAGACCTACTGTGGGAGAGACAAACTAGAGACTCCAAGA	199503
QY	7201	GGAGTGCATTTATGAGCTCTTTCATGTTTCAGGAGAGAGTTGAACCTTAACATAGAAAT	7260
Db	199504	GGAGTGCATTTATGAGCTCTTTCATGTTTCAGGAGAGAGTTGAACCTTAACATAGAAAT	199563
QY	7261	GCCTCAGCAACTCCTGTGATTTAGCCTCTCTGTTCATTTCCCTCAAAAGATTTCCCAT	7320
Db	199564	GCCTCAGCAACTCCTGTGATTTAGCCTCTCTGTTCATTTCCCTCAAAAGATTTCCCAT	199623
QY	7321	TTAGGTTTCTGAGTTCCTGCATGCGGTGATCCCTAGCTGTGACCTCTCCCTCGGAAGTG	7380
Db	199624	TTAGGTTTCTGAGTTCCTGCATGCGGTGATCCCTAGCTGTGACCTCTCCCTCGGAAGTG	199683
QY	7381	TCCTTCATGACCTCAAGCTGCATCTAGAGCTTCCTGATTTCCCTCCCTCAGCTCAGAG	7440
Db	199684	TCCTTCATGACCTCAAGCTGCATCTAGAGCTTCCTGATTTCCCTCCCTCAGCTCAGAG	199743
QY	7441	ACATACACCTATGCTAATTTCAATTTCTTATTTTGGAAAGAGGACTCTTAATTTGGGGA	7500
Db	199744	ACATACACCTATGCTAATTTCAATTTCTTATTTTGGAAAGAGGACTCTTAATTTGGGGA	199803

QY	4561	AGGTTGCAGGGCACGGAATCCCTGTTGGAGTTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Db	196864	AGGTTGCAGGGCACGGAATCCCTGTTGGAGTTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	196923
QY	4621	TCCAAATTTCTGGGAAGGAGCTTTCTCAATCCTAGAGTCTCACTCTATAAATGAGATGTA	4680
Db	196924	TCCAAATTTCTGGGAAGGAGCTTTCTCAATCCTAGAGTCTCACTCTATAAATGAGATGTA	196983
QY	4681	TGAGACAGCCACAAGTCATGGTTTAAATTTCTTTTCCCATGCATATGGCTCAAAAGGAA	4740
Db	196984	TGAGACAGCCACAAGTCATGGTTTAAATTTCTTTTCCCATGCATATGGCTCAAAAGGAA	197043
QY	4741	GTGCTATGGCCCTTGCTTTTTATTAAACCAATAAATCTTTGTATATTTATACTCTTAA	4800
Db	197044	GTGCTATGGCCCTTGCTTTTTATTAAACCAATAAATCTTTGTATATTTATACTCTTAA	197103
QY	4801	AAATTCAGAAATGTCAAGCGCGGCACGGTGGCTCAACCTGTAAATCCAGCAGCTTTGGG	4860
Db	197104	AAATTCAGAAATGTCAAGCGCGGCACGGTGGCTCAACCTGTAAATCCAGCAGCTTTGGG	197163
QY	4861	AGGCGGAGCGGGTGGTCAACAAGTTCAGGAGTTTGAGACAGAGCTGACCAACATGTTGAA	4920
Db	197164	AGGCGGAGCGGGTGGTCAACAAGTTCAGGAGTTTGAGACAGAGCTGACCAACATGTTGAA	197223
QY	4921	ACCGCTCTCTAAAAAATACAAAAATTTAGCTGGTCAAGTCAAGTCAAGTCAAGTCAAGT	4980
Db	197224	ACCGCTCTCTAAAAAATACAAAAATTTAGCTGGTCAAGTCAAGTCAAGTCAAGTCAAGT	197283
QY	4981	GCTAATTTGGAAGGCTGAGGAGGAGCATCGCTTTGAACCTGGGAAGCGGAAGTTGCACTGA	5040
Db	197284	GCTAATTTGGAAGGCTGAGGAGGAGCATCGCTTTGAACCTGGGAAGCGGAAGTTGCACTGA	197343
QY	5041	GCCAAGATCGGCCACTTGCACCTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAA	5100
Db	197344	GCCAAGATCGGCCACTTGCACCTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAA	197403
QY	5101	AAAAAATAAAAAAAGAGAAATTCAGAGATCTCAGATATCATATCAATACCAGGACAAA	5160
Db	197404	AAAAAATAAAAAAAGAGAAATTCAGAGATCTCAGATATCATATCAATACCAGGACAAA	197463
QY	5161	ATATCAAGTGGGCCACTTATCAGAGTAGAGAAATCCTTTAGTTTAAAGTTTCTTTTCAAT	5220
Db	197464	ATATCAAGTGGGCCACTTATCAGAGTAGAGAAATCCTTTAGTTTAAAGTTTCTTTTCAAT	197523
QY	5221	AGAACATAGCAATTAATCACTTGAAGTACCTATCTTCAAGTCGGCTTCTATAACAAATGC	5280
Db	197524	AGAACATAGCAATTAATCACTTGAAGTACCTATCTTCAAGTCGGCTTCTATAACAAATGC	197583
QY	5281	CTCCTAGTTTGACCCAGGTGAAACTGACCAATCTGTAATTCATATTCATGCAACATAA	5340
Db	197584	CTCCTAGTTTGACCCAGGTGAAACTGACCAATCTGTAATTCATATTCATGCAACATAA	197643
QY	5341	AGGGCAATTTTATCTATCAAGCAAAAGACATGGGTAAACAGATATGTATATTACATGTG	5400
Db	197644	AGGGCAATTTTATCTATCAAGCAAAAGACATGGGTAAACAGATATGTATATTACATGTG	197703
QY	5401	AGGAAACAAGCTGATCTGACTGCTCTCCAAGTGAACACTGTTTAGTGTCCAACTTAGG	5460
Db	197704	AGGAAACAAGCTGATCTGACTGCTCTCCAAGTGAACACTGTTTAGTGTCCAACTTAGG	197763
QY	5461	ACACAAATGCTCTCTCTGTAGCTTTTCTTCTGAAAAGGGTATTTCTCTCTCTCC	5520
Db	197764	ACACAAATGCTCTCTCTGTAGCTTTTCTTCTGAAAAGGGTATTTCTCTCTCTCC	197823
QY	5521	AACCTATAGAAGGAAGTGAAGTTCACAGTCTCTCTGGCAAGGGTAAACAGATCCCTCTC	5580
Db	197824	AACCTATAGAAGGAAGTGAAGTTCACAGTCTCTCTGGCAAGGGTAAACAGATCCCTCTC	197883
QY	5581	CTCATCTCTCTCTCTCTGTCAGTGCCTCTCTTTGGTGAAGGTGACATCATGTGACC	5640
Db	197884	CTCATCTCTCTCTCTCTGTCAGTGCCTCTCTTTGGTGAAGGTGACATCATGTGACC	197943

QY	5641	TCTTCAGTGAACACACTCTACGGTGTCGGGCCPTGAACTACTACCCCGAACAACATCACCATTG	5700
Db	197944	TCTTCAGTGAACACACTCTACGGTGTCGGGCCPTGAACTACTACCCCGAACAACATCACCATTG	198003
QY	5701	AAGTGGCTGAAGGATAAGCACGCCCAATGGATGCCAAGCAGTTGC AACCTTAAGACGTATTGG	5760
Db	198004	AAGTGGCTGAAGGATAAGCACGCCCAATGGATGCCAAGCAGTTGC AACCTTAAGACGTATTGG	198063
QY	5761	CCCAATGGGGATGGGACCTAC CAGGGCTGGATAACCTTGGCTGTACCCCTGGGGGAAGAG	5820
Db	198064	CCCAATGGGGATGGGACCTAC CAGGGCTGGATAACCTTGGCTGTACCCCTGGGGGAAGAG	198123
QY	5821	CAGAGATATACGTTNCCAGGTGGACACCCAGGCTCGATCAGCCCCCTCATTTGTGATCTGG	5880
Db	198124	CAGAGATATACGTTNCCAGGTGGACACCCAGGCTCGATCAGCCCCCTCATTTGTGATCTGG	198183
QY	5881	GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGTGTGAGAGGAGTGCC	5940
Db	198184	GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGTGTGAGAGGAGTGCC	198243
QY	5941	TCAGGAGTAAATATGCGACGTGAGATCAGGATCTGCTTTGTTAGGGGTGGGCTGAGG	6000
Db	198244	TCAGGAGTAAATATGCGACGTGAGATCAGGATCTGCTTTGTTAGGGGTGGGCTGAGG	198303
QY	6001	GTGGCAATCAAGGCTTTAACTCTCTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC	6060
Db	198304	GTGGCAATCAAGGCTTTAACTCTCTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC	198363
QY	6061	TAGTCATGGAGTCAATCAGTGGAAATGCTGTTTTGTCGTCATCTTTGTTCAATTGGAATTT	6120
Db	198364	TAGTCATGGAGTCAATCAGTGGAAATGCTGTTTTGTCGTCATCTTTGTTCAATTGGAATTT	198423
QY	6121	TGTTTCATAAATTAAGGAAGAGCAGGGTTCAAGTCAGTAGGAAACAAGGGGAGCTCTCT	6180
Db	198424	TGTTTCATAAATTAAGGAAGAGCAGGGTTCAAGTCAGTAGGAAACAAGGGGAGCTCTCT	198483
QY	6181	TAGTACCTCTGCCCGAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	6240
Db	198484	TAGTACCTCTGCCCGAGGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	198543
QY	6241	AAGCATTTTCTCATTTATATCTTTGGGACACACAGCAGCTCCCTGGGAGACAGAAAT	6300
Db	198544	AAGCATTTTCTCATTTATATCTTTGGGAGACACAGCAGCTCCCTGGGAGACAGAAAT	198603
QY	6301	AATGGTTCTCCCAGAATGAAAGTCTCTAATTCACAAAAATCTTCAGAGCACCTACTAT	6360
Db	198604	AATGGTTCTCCCAGAATGAAAGTCTCTAATTCACAAAAATCTTCAGAGCACCTACTAT	198663
QY	6361	TTTCCAAGAGCTGTTTAAGTACTACAGGGCTTTT GAGGTTGAGAAGTCACCTGTGGCTAT	6420
Db	198664	TTTCCAAGAGCTGTTTAAGTACTACAGGGCTTTT GAGGTTGAGAAGTCACCTGTGGCTAT	198723
QY	6421	TCTCAGAACCCCAATCTGTTAGGGAATGAAATTTGATAGCAAGTAAATGTAGTTAAAGAAG	6480
Db	198724	TCTCAGAACCCCAATCTGTTAGGGAATGAAATTTGATAGCAAGTAAATGTAGTTAAAGAAG	198783
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US-08-724-394A-22
; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
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OTHER INFORMATION: /note= "HLA-H. CONTIG"
US-08-724-394A-22

Query Match 100.0%; Score 10823; DB 2; Length 246240;
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Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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